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SEARCH REQUEST FORM

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ABB80017
     Butler CR,
Karlsson L,
                                                                  06-SEP-2000;
10-AUG-2001;
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HIV-1 vaccine synt	chimeric	ric	peption	tide epi	T/B cel	ic T	æ	CLTB-56/P24M chime	chim	1 vaccine	chimeric	epi	μ.	consensu		-1 p24 epitope	protein T-Cel	DR 3a motif g	DR 3a motif	ccine syn	gag protein	-1 peptide epi	r-helper dete	l epitope, P	1, gag 357-370	B27 super mot	B27 super mot	protease clea	HIV B27 super moti	an immunodefi	tease peptide.	858 super mot	A02 Sup	HIV A03 motif gag

ALIGNMENTS

Cathepsin S; antiallergic; antiasthmatic; dermatological; atopic allergy; hay fever; asthma; atopic dermatitis; foor allergy; dust; pollen; mold; pet dander; pet hair. 05-SEP-2001; 2001WO-US27429 14-MAR-2002. WO200220011-A2 Key Modified-site Unidentified Cathepsin S inhibition assay substrate peptide 17-JUL-2002 ABB80017; ABB80017 standard; peptide; 10 AA (first entry) Location/Qualifiers /note= "C-terminal amide"

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Cai H, Edwards JP, Grice CA, (Khatuya H, Meduna SP, Pio BA,

Gu ı, Sehon (

Gustin on CA, S

2000US-230407P. 2001US-0927324.

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RESULT 2
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1 RL, Wei
                    allergic conditions, allergies, comprises
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                              The present sequence is a peptide used as substrate for a cathepsin S inhibition assay. The Km for the substrate is around 5 uM but the presence of substrate inhibition makes kinetic analysis difficult. With 20 uM substrate, the assay rate is linear over the range of 1-8 ng cathepsin S in 100 ul reaction. Using 2 ng/well of cathepsin S, the production of product is linear and yields about 7-fold signal after 20 min with only 20% loss of substrate. Primary assays are run by quenching the
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other assays, measurements are taken
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                    loss of substrate. Primary assays are run by quenching the reaction after 20 min and then measuring the fluorescence.
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                                                                                                                                                                                                                       Thurmond
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fever; asthma; food allergy;
fasthmatic; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      assay
          every min
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.034;
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                                                                                                                                                              an allergic condition, food allergy
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            for 20
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the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 11;
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percent

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                    score greater than or equal to the score of the result bein and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by score greater than or equal to the score of the
                                                                                                                                                                                                                                                                                                     Score
100.0
100.0
100.0
86.4
86.4
86.8
81.8
81.8
79.5
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Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gapop 10.0 , Gapext 0.5
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIDSI/gcgdata/geneseq/geneseqp-embl/AA1989_DAT:

/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1989_DAT:

/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1990_DAT:

/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1991_DAT:

/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1992_DAT:

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/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1994_DAT:

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/SIDSI/gcgdata/geneseq/geneseqp-embl/AA191.DAT:*
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AAU80096
ABB76233
AAU83139
AAG67257
AAB94593
                                                     AAY74532
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Neisseria gonorrhe
Neisseria meningit
Neisseria meningit
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Human cathepsin S
Substrate for cath
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Amino acid sequenc
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HIV-1 vaccine synt	889	20	34	9	35	45
HIV1 chimeric p	AAY39723	20	34	9.	ω U	44
	972	20	34	9	3 5	43
	9	19	34	9	ω G	42
ide	~	19	34	9	35	41
	587	18	34	٥.	35	40
T/B o	AAW25877	18	34	9.	3 5	39
V3 conse	772	16	34	9	L) G	38
X	AAR68707	16	34	9	3 5	37
\sim	AAR68706	16	34	9	s S	36
HIV-1 vaccine synt	AAW99970	20	32	9	ა 5	35 5
	AAY39767	20	32	9	ω 5	34
	AAW67362	19	32	9	35	33
ic T/B	AAW25846	18	32	9.	35	32
P24M/V3 consensus	AAR68676	16	32	9.	35	31
GAG se	AAU84422	23	30	9	35	30
-1 p24 epito	AAW82529	19	25	9	3 5	29
protei	AAR07981	11	24	9	35	28
DR 3a mot	ABP24915	22	15	9	35	27
DR 3a motif	ABP24909	22	15	9	35	26
1 vaccine	AAW98894	20	15	9	35	25
1 gag prote	967	20	15	9.	3 5	24
-1 peptide e	739	19	15	9.	35	23
T-hel	8	18	15	9	35 5	22
ell epitope	870	16	15	9.	35	21
1, gag 357-	w	13	14	9.	35	20
B27 super	ABP17220	22	12	٩	35	19
B27 super	_	22	12	9.	35	18
protease o	8	18	12	9	ω 5	17
=	ABP17190	22	11	9	35	16
an immunod	579	23	10	9	35 5	15
tease pepti	1911	ະນີ	۱ آو	9	35	14
B58 super	1796	22	9	9.	ა 5	13
A02 super m	P1275	25	9	79.5	35	12
HIV A03 motif qa	ABP20832	22	8	9	35	11
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ALIGNMENTS

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ABB80017
ID ABB80017
ID ABB8
XX
AC ABB8
XX
DT 17---
XX
Cath
X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cathepsin S; antiallergic; antiasthmatic; dermatological; pyrazole; atopic allergy; hay fever; asthma; atopic dermatitis; food allergy; allergy; dust; pollen; mold; pet dander; pet hair.
Butler CR,
Karlsson L,
                                                                                                                                                                                                                                       06-SEP-2000; 2000US-230407P.
10-AUG-2001; 2001US-0927324.
                                                                                                                                                                                                                                                                                                                                                                          05-SEP-2001; 2001WO-US27429.
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                                                                                                                                            (ORTH ) ORTHO-MCNEIL PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB80017 standard; peptide; 10 AA
Cai H, Edwards JP, Grice CA, G
Khatuya H, Meduna SP, Pio BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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u Y, Gustin
Sehon CA, S
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RESULT 2
AAU80096
AD AAU80096
AC AAU8
AC AAU8
AC AAU8
AC Cath
KW Cath
KW Food
AX Synt
ET Mod1

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Best Local
                                         Treating allergic conditions, and food allergies, comprises
                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to the treatment of allergic conditions, comprising the administration of a pyrazole derivative. The activity of derivatives of the invention may be described as, antiallergic, antiasthmatic and dermatological. They act as cathepsin S inhibitors and may be used for the treatment of allergic conditions including atopic allergies, e.g. hay fever, asthma, atopic dermatitis, food allergies and allergies to dust, pollen, mold, pet dander or pet hair. The current sequence represents a cathepsin S inhibition assay substrate peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tays
                                                                                                                                                                                   Cai H,
                                                                                                                                                                                                                                                                       06-SEP-2000;
10-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cathepsin S
                                                                                                                                                            Thurmond
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                                                                                                                                                                                                                           (ORTH ) ORTHO-MCNEIL PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
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10; Conser
                                                                                                                                                         Edwards JP,
1 RL, Wel J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54; Page 134; 165pp; English
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2001US-0927188.
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Pred. No.
                                            e.g. hay fever, administration
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                                         fever, asthma, atopic or
ration of a substituted
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RESULT 3
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The present sequence is a peptide used as substrate for a cathepsin S inhibition assay. The Rm for the substrate is around 5 uM but the presence of substrate inhibition makes kinetic analysis difficult. With 20 uM substrate, the assay rate is linear over the range of 1-8 ng cathepsin S in 100 ul reaction. Using 2 ng/well of cathepsin S, the production of product is linear and yields about 7-fold signal after 20 min with only 20% loss of substrate. Primary assays are run by quenching the reaction after 20 min and then measuring the fluorescence. For other assays, measurements are taken every min for 20 min. The rate is calculated from the slope of the increase and the percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         comprising administration of a composition comprising a substituted pyrazole (I) or a salt, amide or ester. The method is used for treating allergic conditions, e.g. hay fever, asthma, atopic dermatitis and food allergies. The present sequence represents human cathepsin S substrate peptide used in an assay to demonstrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cathepsin S; inhibitor; allergy; hay fever; asthma; atopic dermatitis; antiallergic; antiasthmatic; dermantiinflammatory; immunosuppressive.
                                                                                                                                                                                                                                                                                                       Example 1;
                                                                                                                                                                                                                                                                                                                                                     Use of cathepsin S inhibitor for treating hay fever, asthma, atopic dermatitis or a
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RESULT 4
AAU83139
               The invention describes an isolated mammalian secreted polypeptide (MSP) CC (II) (I) is useful to direct the secretion of other proteins of interest from a host cell, to monitor secretion of proteins, to degenerate comparising all nucleotide sequences encoding a particular polypeptide, to screen for cell metabolism effecting receptors, for identifying new target receptors and drug design, for identifying, for comparising the weight of expressed MSP comparisities as a ratio to total protein expressed, for identifying polypeptides as a ratio to total protein expressed, for identifying polypeptides as a ratio to total protein expressed, for identifying comparison acid sequence analysis, for monitoring biological activities of the protein in vitro and in vivo, and to teach analytical skills and as reagents for the study of cells, receptors, and other binding molecules. The polynucleotide is useful for radiation hybrid mapping, and somatic contiguous maps of mammalian chromosomes. Reagents disclosed in the contiguous maps of mammalian chromosomes, Reagents disclosed in the over or under production of the protein. This is the amino acid sequence of a mammalian secreted polypeptide, described in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated mammalian secreted polypeptide useful in therapeutic and diagnostic methods, to direct secretion of other proteins of interest from host cell, as educational tools, and as laboratory practicum kits
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invention
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27-AUG-1999;
18-OCT-1999;
                                                                            The present sequence is encoded by a liver associated gene. The expression level of this gene changes in liver (hepatic) cancer. Liver associated gene can be used as markers in blood tests for screening for the early stages of the liver cancer. The encoded proteins and peptides can also be used as targets for screening for compounds to treat the disease. They can also be used for predicting the progress of the disease.
                                                                                                                                                                             New genes and their proteins found in hepatic cancer, vectors, antibodies, and screening method for compounds with binding ac useful as diagnostics and targets for treatment agents .
                                                           Sequence
                                                                                                                                                            Claim 1;
                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                              09-JUN-2000;
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02-MAY-2000;
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  1 EKARVLAEAA 10
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2 EKSRLLAEAA 61
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DB; AAH77810.
                    Similarity
8; Conserv
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8; Conser
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                                                                                                                                                                                                                                                                       Isogai T,
                                                                                                                                                           Page 79-80;
                                                                                                                                                                                                                                                  Sugiyama T
Hippo Y,
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                                                           396 AA;
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99US-0159590
2009UP-0118776,
2000US-0183322
2000UP-0183767,
2000UP-0241899
                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene; hepatic cancer; liver cancer; marker.
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a T, Wakamatsu A
Y, Taniguchi H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
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80.0%;
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                    Score 38; DB Pred. No. 19; 2; Mismatches
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Pred.
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A, Nagai K,
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11;
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19;
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(, Otsuki
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RESULT 6
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PF 28-J
PR 29-J
PR 11-J
PR 11-J
PR 12-J
                                                                                                                                                                                                                                                                              The present invention describes primer sets for synthesising 5602 CC full-length cDNAs defined in the specification. Where a primer set CC comprises: (a) an oligordT primer and an oligonucleotide comprises one of the 5602 nucleotide sequences defined in the specification, where the CC cligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the CC complementary strand of a polynucleotide which comprises a 5'-end cC sequence and an oligonucleotide comprising a sequence, where the CC oligonucleotide which comprises a 3'-end sequence, where the CC oligonucleotide comprises a 3'-end sequence, where the CC oligonucleotide comprises a 3'-end sequence, where the 10 septimers are useful for synthesising polynucleotides, of the 5'-end sequence/3'-end sequence is selected from those defined in CC the specification. The primer sets can be used in antisense therapy and CC in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH1372 represent human cDNA sequences; AAB92446 to cahes of the present oligonucleotides, all of which are used in the exemplification of the present oligonucleotides, all of which are used in the exemplification.
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В
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Best Local :
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
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                                                                                                                                                                                                                                    Sequence
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   229
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                                                      EKARVLAEAA 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; SEQ ID 15405; 2537pp + CD ROM;
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                                                                                                               8; Conserv
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99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                     Conservative
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T, Wakamatsu
                                                                                                                                             86.4%;
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A, Nagai K,
                                                                                                                                             No.
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19;
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Otsuki
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RESULT 7
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XX Neis
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Matches 7
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31-JUL-1998;
02-SEP-1998;
02-SEP-1998;
09-OCT-1998;
09-OCT-1998;
09-OCT-1998;
25-FEB-1999;
                                                                                                                                                                                                                             AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ54473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fraser C,
Petersen i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel Neisserial polypeptides vaccines and diagnostics -
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                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
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DB; AAZ53293.
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                                                                                                                Similarity
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Venter JC;
                                                                                             Conservative
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98US-009486

98US-0098994

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98US-0103749

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98US-0121528
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77.8%;
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Rappuoli R,
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Pred. No.
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Ratti
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meningitis; septicaemia;
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Scalato E, Scarselli
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02-SEP-1998;
02-SEP-1998;
09-OCT-1998;
09-OCT-1998;
09-OCT-1998;
25-FEB-1999;
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(GENO-)
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                                                                                                                                                                                                                                                                                                        Sequence
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Tettelin H,
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                                                                                                      11 DKARILAEA 19
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DB; AAZ53294.
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7; Conserv
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INST GENOMIC
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, Pizza M, Rappuoli R,
, Venter JC;
                                                                                                                                                                                                                                                                                                        298 AA;
                                                                                                                                                                                                       Conservative
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98US-0094869.
98US-00998994.
98US-0099062.
98US-0103794.
98US-0103794.
98US-0103794.
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                                                                                                                                                                                                                               81.8%;
77.8%;
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                                                                                                                                                                                                  Score 36; DB Pred. No. 36; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hickey E,
Ratti G,
                                                                                                                                                                                                                                                    21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      be useful antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antigen; vaccine;
meningitis; septicaemia;
                                                                                                                                                                                                    0,
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Scalato E, S
                                                                                                                                                                                                                                                      Length 298;
                                                                                                                                                                                                    Indels
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Scarselli M;
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RESULT 10
ABP12631
ID ABP12
XX
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Вþ

11

DKARILAEA

ABP12631 standard; Peptide;

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Qy
                           Matches
                                        Query Match
Best Local
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Petersen J,
Tettelin H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-OCT-1998;
09-OCT-1998;
09-OCT-1998;
25-FEB-1999;
                                                                                                   represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ54737 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia; antibacterial; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1998;
31-JUL-1998;
                                                                                                                                                                                                                                                                                             Claim 2; Page 392; 1453pp; English.
                                                                                                                                                                                                                                                                                                                    Novel Neisserial polypeptides predicted to vaccines and diagnostics -
                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CHIR )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-SEP-1998;
02-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY74533 standard; Protein; 298 AA.
                                                                              Sequence
                                                                                                                                                                                                                                                                  AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941
                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09957280-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria meningitidis ORF 138 protein sequence SEQ ID NO:540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-APR-1999;
  1 EKARVLAEA 9
                                                                                                                                                                                                                                                                                                                                                               2000-062150/05.
DB; AAZ53295.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHIRON CORP.
INST GENOMIC RES.
                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                Galeotti C, Grandi G,
, Pizza M, Rappuoli R,
, Venter JC;
                                                                                298
                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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98US-0099062.
98US-0103749.
98US-0103794.
98US-0103796.
99US-0121528.
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98US-0094869.
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                                        81.8%;
77.8%;
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N
                                        Score 36; DB Pred. No. 36;
                             Mismatches
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Ratti
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                                                    21;
                                                                                                                                                                                                                                                                                                                                    be useful antigens
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Scalato E, Scarselli
                                                   Length 298;
                             Indels
                             0
                          Gaps
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RESULT 11
ABP20832
ID ABP20
XX
AC ABP20
XX
DT 15-Ju
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Best Local Similarity
Watches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a composition (I) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABL25347 to ABP25397). (I) has virucide activity and can be used in vaccines. (I) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sette A,
Baker DM,
                                                                                                                                                                                                                                                                                                                                 escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABPIIS01 to ABP25412 represent peptide sequences used in the exemplification of the present
   15-JUL-2002
                                  ABP20832;
                                                                  ABP20832 standard;
                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-OCT-2000; 2000WO-US27766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200124810-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1 -
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                                                                                                                                                      _
                                                                                                                                                                                     2 KARVLAEA 9
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Celis E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 127; 448pp; English.
                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                       Conservative
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 (first entry)
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                                                                  Peptide;
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                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                   Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 S, Livir
Grey HM;
                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                     DB 22;
7.8e+05;
                                                                                                                                                                                                                                                 Length 8;
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RESULT 12 ABP12751

ABP12751 standard; Peptide;

9

0

SEXEXEX

ABP12751;

15-JUL-2002 (first entry)

HIV A02 super motif gag peptide #222

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В
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                                                                     Matches
                                Query Match
Best Local
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Baker DM,
                                                                                                                                                                                                                         Claim 32; Page 296; 448pp; English.
                                                                                                                                                                                                                                                                                                                                                                            HIV: HIV-1; human immunodeficiency virus; env; pol: gag; nef; vpr; vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.
                                                                                                                                                                                                                                     Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1 -
                                                                                                                                                                                                                                                           WPI; 2001-354887/37.
                                                                                                                                                                                                                                                                                                          05-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                     12-APR-2001
                                                                                                                                                                                                                                                                                                                                                               Human immunodeficiency virus type 1.
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                                                                                                                                                                                                                                                                                             (EPIM-) EPIMMUNE INC
1 KARVLAEA
            2 KARVLAEA 9
                         Similarity
8; Conser
                                                                                                                                                                                                                                                                        Sidney J,
Celis E,
                                                    8
                         Conservative
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8
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                                79.5%; Score 35; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                        Southwood S, Livi
Kubo RT, Grey HM;
                          <u>.</u>
                           Mismatches
                                                                                                                                                                                                                                                                              Livingston BD,
                          DB 22; 1
7.8e+05;
hes 0;
                                      Length 8;
                           Indels
                                                                                                                                                                                                                                                                               Chesnut
                          0
                          Gaps
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RESULT 13
ABP17961
ID ABP17
XX ABP17
AC ABP17
XX 15-JU
XX 15-JU
XX HIV B
XX HIV:
KW AD1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               CC The present invention describes a composition (1) comprising a prepared CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid Sequences calected from 51 defined amino acid sequences (ABL25347 to CC ABP25397). (1) has virucide activity and can be used in vaccines. (1) CC may be used for immunising subjects against HIV-1 infections. The use of Group-based vaccines has several advantages over traditional vaccines (CC compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen. (CC allowing for immune escape due to mutations. The groups for inclusion in CC an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of CC escape mutants. Furthermore, immunosuppressive groups that may be present CC in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the CC immunogenicity. Accordingly, the immune response can be modulated, as CC appropriate, for the target disease. Similar engineering of the response CC invention.

CC invention.
                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                    Query Match
HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; e antigen; vaccine; HIV infection; immunisation; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HIV: HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.
                                                                                                                                            ABP17961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-OCT-1999;
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                                                                  HIV B58 super motif gag peptide #180
                                                                                                          15-JUL-2002
                                                                                                                                                                         ABP17961 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                          invention
                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                 1 KARVLAEA 8
                                                                                                                                                                                                                                                                                               2 KARVLAEA 9
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Celis E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 130; 448pp; English
                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        A
                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0412863
                                                                                                                                                                                                                                                                                                                                                    79.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kubo RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Southwood S, Livingston BD, Kubo RT, Grey HM;
                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                  Score 35; DB 22;
Pred. No. 7.8e+05;
                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                  Length 9;
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RESULT 14
AAE19118
ID AAE19
XX AAE19
AC AAE19
AC AAE19
XX Z1-MA
DT 21-MA
DT 21-MA
XX Lucii
KW cell
XX Cell
XX Unide
XX Unide
XX WO200

Protease peptide 21-MAY-2002 AAE19118;

(first entry)

AAE19118 standard; peptide;

10

Luciferase; cell death.

enzyme;

protease; cell growth; apoptosis; therapeutic;

WO200206458-A2

Unidentified

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CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid compensation of the virus-1 (HIV-1) group comprising an amino acid composition of the use of CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) CC may be used for immunising subjects against HIV-1 infections. The use of CC group-based vaccines has several advantages over traditional vaccines, CC particularly when compared to the use of whole antigens in vaccines compositions. There is evidence that the immune response to whole callowing for immune escape due to mutations. The groups for inclusion in CC allowing for immune escape due to mutations. The groups for inclusion in CC escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced as a compropriate, for the target disease. Similar engineering of the response can be modulated, as corresponse to the persons of the present persons that traditional approaches. ABP11501 to ABP25412
                                   Query Match
Best Local :
                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                     sequence selected from 51 defined amino acid ABP25397). (I) has virucide activities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-354887/37
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                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Baker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (EPIM-) EPIMMUNE INC
                                                                                                                       Luveution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present invention describes a composition (I) comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32; Page 237; 448pp; English.
                 Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sidney J,
Celis E,
                                                                                      9
                   Conservative
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100.0%; Score 35;
100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Southwood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S, Livingston Grey HM;
                   Mismatches
                                   DB 22;
7.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BD,
                                               Length 9;
                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chesnut
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                   Gaps
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24-JAN-2002

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RESULT 15
AAU75795
XX
AC AAU75
AC AAU75
XX
DT 08-MJ
XX
DE Huma
XX
Gag
KW Gag
KW Prot
KW huma
XX
FH Key
FT Cle
FT
XX
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC The invention relates to a purified polypeptide having luciferase CC activity and a recognition site specifically cleavable by a protease, CC where cleavage results in a decrease in luciferase activity. The CC polypeptide comprises a localisation sequence which is linked to the CC luciferase polypeptide by the cleavable recognition sequence. The CC luciferase polypeptide by the cleavable recognition sequence. The CC modulator, an inhibitor of apoptosis and for detecting luciferase activity in a sample. The polypeptide is used for characterising and CC identifying cellular processes associated with metabolism, cell growth CC and cell death e.g. apoptosis and for measuring protease activity. The CC and cell death e.g. apoptosis and for measuring protease activity. The CC cellular biochemical pathways are useful for characterising, identifying CC cellular biochemical pathways as well as identifying diagnostic and CC determining amount of protease in a sample and for monitoring the cCC activity of protease inside a cell that expresses a recombinant collections. The present sequence is a protease peptide used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leng
                    WO200210430-A2
                                                                    Cleavage-site
                                                                                                                   Human immunodeficiency
                                                                                                                                                Gag protein; antiviral; nucleic acid construct; viral protease; protease recognition site; PRS; viral drug resistance; HIV; human immunodeficiency virus.
                                                                                                                                                                                                                  Human immunodeficiency virus Gag protein protease cleavage sequence
                                                                                                                                                                                                                                                       08-MAY-2002
                                                                                                                                                                                                                                                                                      AAU75795;
                                                                                                                                                                                                                                                                                                                  AAU75795 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-195809/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CHEM-) CHEMICON INT INC
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8; Conserv
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                                                                                                                                                                                                                                                      (first entry)
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                                                                    Location/Qualifiers 5
                                                     /label= HIV_protease_cleavage_site
                                                                                                                     virus
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1.7;
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Search completed: March 13, Job time: 27.5455 secs

2003, 18:49:14

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KARVLAEA

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CC and a protease, where cleavage of the PRS lelavable by a virally encoded CC protease, where cleavage of the PRS leads to a detectable signal. The CC nucleic acid construct of the invention is useful for uncovering CC molecules having antiviral activity or for determining viral drug CC resistance and the chimeric peptide is also useful for detecting the CC presence of a virus in a cell. Other uses of the invention are detecting to researce of viral infection. The nucleic acid construct is useful for CC phenotypic testing of human immunodeficiency virus (HIV) drug resistance. CC The invention enables screening of molecules in an easy and rapid manner CC and allows efficient detection of the presence of viral protease and CC viral particles within cells. The construct is specific, sensitive and CC lacks background enzymatic activity in the absence of human CC immunodeficiency virus protease, and is suitable for detection of CC specific viral strain isolates even under low viral load conditions. When used for phenotypic testing of HIV drug resistance it delivers accurate cresuits within 24 hours. The present amino acid sequence represents one of several (AAU75794-AAU75798) HIV Gag protein protease cleavage
                                     Query Match
Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a new nucleic acid construct that comprises a polynucleotide cassette encoding a chimeric polypeptide comprises a first polypeptide sequence, a second polypeptide sequence translationally fused to the first sequence,
                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid construct for detecting anti-viral drugs, comprises polynucleotide cassette encoding a chimeric polypeptide with two polypeptide sequences and a protease recognition site cleavable by a virally encoded protease
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2 KARVLAEA 9
                                        Similarity
8; Conserv
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                                                        79.5%;
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                                     Score 35; DB; Pred. No. 1.7
0; Mismatches
                                                                                  DB 23;
                                          0;
                                                                             Length 10;
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
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seq length:
  Match
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 Issued_Patents_AA:*
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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                  US-08-792-553-4
US-09-63-941-15
US-09-817-413-15
US-09-817-43-15
US-09-147-208-21
US-08-460-6028-76
US-08-465-2178-76
US-08-465-2978-76
US-08-465-2978-76
US-08-465-5078-47
US-08-465-2178-47
US-08-465-2178-47
US-08-465-2178-47
US-08-465-2178-47
US-08-465-2178-47
US-08-465-2577-47
US-08-463-3968-78
US-08-463-3968-77
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US-08-463-9688-78
US-08-463-9688-78
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ALIGNMENTS

RESULT 1

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FILING DATE: 31-JAN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Haile, Ph.D.:
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07257/041001/UC 96-160-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEPAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                 US-08-792-553-4
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                                                                                                           Query Match
                                                                          Matches
                                                                                                                                                                 LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Tsien, Roger Y.
APPLICANT: Heim, Roger
TITLE OF INVENTION: Tandem
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 4225 Exc
CITY: La Jolla
STATE: Californ
COUNTRY: USA
MEDIUM TYPE:
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                                                                        Local Similarity les 8; Conserv
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                                                                      79.5%; Score 35; DB 2; llarity 100.0%; Pred. No. 0.36; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     umber: US/08/792,553
31-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
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Suite 1400
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VOLUME: 38
; PAGES: 299-
; DATE: 1974
US-09-053-941-15
              RESULT 4
US-09-147-208-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -Sequence 15; Application US/09817413
    Patent No. 6436648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: SRINIVISAN, ALGARSAMY
APPLICANT: KOPROWSKI, HILARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
Sequence 21, Application US/09147208
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
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Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SRINIVISAN, ALGARSAMY
APPLICANT: KOPROWSKI, HILARY
TITLE OF INVENTION: CHIMERIC VIRAL PROTEINS
FILE REFERENCE: Chimeric Viral Proteins
CURRENT APPLICATION NUMBER: US/09/053,941
CURRENT FILING DATE: 1998-04-02
EARLIER APPLICATION NUMBER: 60/043,380
EMARLIER FILING DATE: 1999-04-03
                                                                                                                                                                                                                       ORGANISM: Human immunodeficiency virus type PUBLICATION INFORMATION: JOURNAL: Meth. Enzymol. VOLUME: 38 PAGES: 299-DATE: 1974
                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/817,413
CURRENT FILING DATE: 2001-03-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: KOPROWSKI, HILARY
TITLE OF INVENTION: CHIMERIC VIRAL PROTEINS
FILE REFERENCE: Chimeric Viral Proteins
                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 1999-04-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Human immunodeficiency virus type PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                    LENGTH: 10
TYPE: PRT
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TYPE: PRT
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Pred. No.
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Pred. No.
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SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: SIA, Ch
APPLICANT: CHONG,
APPLICANT: KLEIN,
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 76, Application US/08257528B Patent No. 5639854
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GENERAL INFORMATION:
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TOPOLOGY: lin
MOLECULE TYPE:
       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION UNMER: US/08/257,528B
FILING DATE: 09-UN-1994
CLASSIFICATION: 424
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/147,208 FILING DATE: 02-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Rudolph, John R.
REGISTRATION NUMBER: 38,003
REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides NUMBER OF SEQUENCES: 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                         COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                                                                                         STREET: Suite
CITY: Toronto
                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
les 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Toronto
                                                                                                                                                                                                                                                                    ADDRESSEE:
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Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                        CHONG, Pele
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                                                                                                                                                                                                                                                                                                                                          KLEIN, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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linear
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416) 361-1398
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Best Local Similarity
Watches 8; Conserv
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 Query Match
                                                                                                                                                                                    APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CCLASSIFICATION 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT IMPORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REGISTRATION NUMBER: 24,973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                    TELEFAX: (416) 595-1163 INFORMATION FOR SEQ ID NO: 76:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: Canada ZIP: M5G 1R7
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                              REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0 FILING DATE: 02-JUN-1995 CLASSIFICATION: 424
                                                         TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Suite CITY: Toronto
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                                                                                        ENGTH:
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                                                                                     15 amino acids
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(70 TO NO: 76:
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                                                         single
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 79.5%;
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 Score 35;
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DB 1;
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Length 15;
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RESULT 8
US-08-465-217A-76
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-UN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
APPLICATION NUMBER: 08/073,378
APPLICATION NUMBER: 09-UN-1993
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APPLICANT: I
                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
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MEDIUM TYPE: Floppy
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NAME: STEWART, MICHAEL I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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3 KARVLAEA 10
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                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-487 MIS:jb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                         3 KARVLAEA 10
                                                                                  2 KARVLAEA 9
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(416) 59
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Suite 701, 330 University Avenue
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KLEIN, Michel H.
                                                                                                               Conservative
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                     linear
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                                                                                                                                                                                                  single
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                                                                                                                             79.5%; Score 35; 100.0%; Pred. No.
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0; Mismatches
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Sequence 76, Application US/0846; Patent No. 5800822; GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele

76, Application US/08465217A o. 5800822

CURRENT APPLICATION DATA:

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Query Match
Best Local Similarity
Thes 8; Conserv
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US-08-465-217A-76
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                                                                                                                                                                                                                                                                              Sequence 76, Applicate Patent No. 5817754
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (416) 595-1155
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: 05-UUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: 08/257,
FILING DATE: 09-UUN-1994
CLASSIFICATION: 424
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DDS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                     TITLE OF INVENTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
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                                                                                                                      STATE:
                                                                                                                                   CITY: Toronto
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OPERATING SYSTEM:
                                                                                                   COUNTRY:
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м5G 1R7
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5817754
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                                                                                                                    Ontario
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Sulte 701, 330 University Avenue
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US-08-462-507A-76
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
                                                                                                                                                                                                                                21P: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 76
                                                                                                                                                            APPLICATION NUMBER: US/01
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
FILING DATE: 09-JUN-1
CLASSIFICATION: 424
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LENGTH: 15 amino acids
TYPE: amino acid
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REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                          ATTORNEY/AGENT INFORMATION:
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NAME: STEWART, MICHAEL I
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 09-JUN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides NUMBER OF SEQUENCES: 101
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                                                                                                                                APPLICATION NUMBER: 08/2 FILING DATE: 09-JUN-1994
                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                     STREET: Suite
CITY: Toronto
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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MSG 1R7
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Suite 701, 330 University Avenue
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                                                           09-JUN-1993
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100.0%;
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                                                                              08/073,378
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Pred. No.
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US-08-467-881A-76
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US-08-467-881A-76
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Query Match 79.5%; Sometive 8; Conservative 0;
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                                                                                                   TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
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INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/073,378
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PRIOR APPLICATION NUMBER: 08/257,528
                                                                                                                                                                                          REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
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NAME: STEWART, MICHAEL I
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STRANDEDNESS: sin
                                                                                      STRANDEDNESS:
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KLEIN, Michel H.
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score 35; DB
pred. No. 0.5
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Pred. No.
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            DB 2;
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Best Local Similarity
Thes 8; Conserv
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US-08-257-528B-47
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US-08-460-602A-47
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                                                                                                                                                                                        Sequence 47, Application US/08460602A Patent No. 5759769
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                                                                                                                                                                             GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/257,528B
                                                                                                                               APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
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NAME: STEWART, MICHAEL I
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                                                                                     CORRESPONDENCE ADDRESS
                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                 TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
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CITY: Toronto
                                         STREET: Suite CITY: Toronto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/0
FILING DATE: 09-JUN-1994
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             COUNTRY:
                             STATE:
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M5G 1R7
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                          Ontario
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Suite 701, 330 University Avenue
                                                       Suite 701, 330 University Avenue
             Canada
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KLEIN, Michel H.
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                                                                        Sim & McBurney
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100.0%; Pr
                                                                                                                  Tandem Synthetic HIV-1 Peptides
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Pred. No
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GENERAL INFORMATION:
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                                             APPLICATION NUMBER: US/08/463,960
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (416) 595-1163 INFORMATION FOR SEQ ID NO:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073
FILING DATE: 09-UN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COETHABER. PATENTIALES
                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
                   PRIOR APPLICATION DATA:
                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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LENGTH: 32 amino acids
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APPLICATION NUMBER: 08/2
FILING DATE: 09-JUN-1994
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Polon-
                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                        ZIP: M5G 1R7
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STRANDEDNESS: sin
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REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-450 MIS:jb
APPLICATION NUMBER:
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Cocal Similarity 100.0%; Pred. No.
S 8; Conservative 0; Mismatch
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                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,217A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
ETILING DATE: 09-JUN-1994
FILING DATE: 09-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 58008
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Best Local
                                                                       TELEFAX: (416) 595-1163 INFORMATION FOR SEQ ID NO:
                                                                                                                         CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
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STRANDEDNESS: single

TOPOLOGY: lin-
           SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
CTRANDEDNECC: atomic
                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, MICHEL H.
TITLE OF INVENTION: Tandem S
NUMBER OF SEQUENCES: 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Suite
CITY: Toronto
STATE: Ontario
                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/0 FILING DATE: 09-JUN-1993
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ZIP: M5G 1R7
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CLASSIFICATION:
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US-08-465-217A-47

OURTY METICAL SIMILARITY 79.5%, Score 35: DB 1; Length 32; BEST LOCAL SIMILARITY 100.0%; Pred. NO.1.2; 0; Indels 0; Gaps 0; OY 2 KANYLARA 9

OY 2 KANYLARA 9

Db 3 KANYLARA 10

Search completed, March 13, 2003, 18:53:52

Job time: 9.90909 secs
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Result
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Listing first 45 summaries
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99.409 Million cell updates/sec
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dict	homo	Q9bx75 homo sapien	Q95kh8 macaca fasc	Q8r4t3 rattus norv	Q961x2 homo sapien	rat	O88346 mus musculu	Q9qup7 mus musculu	homo	O88795 mus musculu	Q923s7 rattus norv	093376 salmo salar	Q9np46 homo sapien	Q9w7a2 coturnix co	mus muscul		meleagris	Q95mc9 canis famil	Q64377 mus musculu	Q64360 mus musculu	\sim	gal	Q9buf6 homo sapien	Q9tum9 bos taurus	Q918r9 mitu toment		Q9de10 mitu toment	Q95mc7 canis famil

ALIGNMENTS

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0978R7; O1-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
N-terminal acetyltransferase complex subunit.
TV1348 OR TVG1394372.
                                                                                                                                       Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S., Kawashima Ohya Y., Wattanabe K., Yamazaki M., Kanehori K., Kawamo Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.; "Archaeal adaptation to higher temperatures revealed by genomic sequence of Thermoplasma volcanium."; proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000). EMBL; AP000996; BAB60490.1; -InterPro; IPR000182; GCN5acetyltransf.
                                                                                                                                                                                                                                                                                                                                        Thermoplasma volcanium.

Archaea: Euryarchaeota; Thermoplasmata; Thermoplasmataceae; Thermoplasma.
                                                                                                          Transferase; Compre
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=GSS1 / DSM 4299 / JCM 9571;
MEDLINE=20570466; PubMed=11121031;
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 49
1 ERAEQQRLKSQD 12
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49 ERAEQERIKSLD 60
                                                       Similarity
9; Conserv
                                                         Conservative
                                                                                                               Complete proteome.
77 AA; 20436 MW;
                                                                   74.2%;
75.0%;
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Pred. No. 1
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RESULT
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01-MAR-2001 (TrEMBLrel. 16, L
01-MAR-2002 (TrEMBLrel. 20, L
Hypothetical protein Ta0277,
TA0277.
  Q90Y46
Q90Y46;
Q1-DEC-2001
01-DEC-2001
                                                                                                                                                                                 Jin J.-P., Blestadecki B.;
"Mutant turkey cardiac troponin T.";
submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AF274301; AAK586B5.1; -
InterPro: IPR001978; Troponin.
Pfam; PF00992; Troponin; 1.
SEQUENCE 281 AA; 33651 MW; 7BF0B960E7674718 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                    Q90ZC6;
                                                                                                                                                                                                                                                                                               Meleagris gallopavo (Common turkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleag
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01-DEC-2001 (TrEMBLrel 19, Las
01-MAR-2002 (TrEMBLrel 20, Las
Low Mr mutant cardiac troponin
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EMBL: AL445063; CAC11422.1; -.

INTERPROVO182; CONSacetyltransf.

Pfam; PF00583; Acetyltransf; 1.

Hypothetical protein; Complete proteome.

Hypothetical protein; Complete 2B12B57CE83C6FDC CRC64;
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STRAIN-DSM 1728;
MEDLINE-20479972; PubMed-11029001;
Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
Reupp A., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
"The genome sequence of the thermoacidophilic scavenger Thermoplasma
acidophilum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermoplasma acidophilum.
Archaea; Euryarchaeota; Thermoplasmata;
Thermoplasmataceae; Thermoplasma.
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Best Local S
Matches 8
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Jin J.-P., Biesladecki ...,
Mutant turkey cardiac troponin T.
Submitted (JUL-2000) to the EMBL/(
EMBL; AY005139; AAG23714.1; -.
InterPro; IPR001978; Troponin.
Pfam; PF00992; Troponin; 1.
Pfam; PF00992; Troponin; 1.
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Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence of the control of the co
                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2002 (TrEMBLrel. 20,
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Deinococcus radiodurans.
Bacteria; Thermus/Deinococcus
Deinococcaceae; Deinococcus.
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Jin J.-P., Biesiadecki B.;
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Cyprinidae; Danio.
NCBI_TaxID=7955;
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                                                                                                                                                           Methyl-accepting
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NCBI_TaxID=9103;
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Eukaryota; Metazoa; Chordata;
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| ERAEQQRIRSE 148
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ERAEQORIRSE 145
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72.7%;
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Last annotation update)
-related protein.
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Pred. No.
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; Craniata; Vertebrata; Euteleostomi;
Teleostei; Ostariophysi; Cypriniformes;
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                                          group;
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SEQUENCE
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Science 286:1571-1577(1999).
EMBL; AE001863; AAF12432.1;
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                                                                                                                                                                                            "Molecular cloning of human cardiac trponin developing and failing heart.";
J. Mol. Cell. Cardiol. 27:223-2236(1995).
EMBL; X79859; CAA56239.1;
                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel 01, 01-NOV-1996 (TrEMBLrel 01, 01-JUN-2002 (TrEMBLrel 21, Troponin T (Fragment)
 Q9Z0X5
                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                 Q15608;
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InterPro; IPR003560; HAMP.
Pfam; PF00672; HAMP; 1.
Pfam; PF00015; MCPsiqna1; 1.
SMART; SM00304; HAMP; 2.
                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-96129582; PubMed-8576938;
                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of the radioresistant bacterium Deinococcus
radiodurans R1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fraser C.M.;
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                                                                                                                                                             InterPro; IPR001978; Troponin. Pfam; PF00992; Troponin; 1. NON_TER 175 175
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756 AA;
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 PRELIMINARY;
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                                                                                                                                                  20918 MW;
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69.28;
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Pred. No.
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Pred. No.
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 PRT;
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                                                                                                     Mismatches
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RX RAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA RAWAI J., Shinagawa A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Sahburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Sahburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schrimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schrimi L., M., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Wayshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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01-JUN-2001
01-JUN-2001
01-JUN-2001
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01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Troponin T (Fragment).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Rodentia; Hystricognathi; Cavildae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Submitted (OCT-1998) to the EM
EMBL; AF099071; AAD16291.1; -
InterPro; IPR001978; Troponin.
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MEDLINE=99345814; PubMed=10409222;
Preisig-Muller R., Mederos y Schnitzler M.,
"Separation of cardiomyocytes and coronary
  Hayashizaki Y.; "Functional annotation of Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Troponin T3, TNNT3.
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Am. J. Physiol. 27
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7; Conserv
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177
177 AA;
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                               full-length
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Pred. No. 14;
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Sciurognathi; Muridae;
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                                 collection.";
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RESULT 11
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Xu Y., He J., Wang X., Lim T.M., Gong Z.;
"Asynchronous activation of 10 muscle-specific protein (MSP) genes during zebrafish somitogenesis.";
Dev. Dyn. 219:201-218(2000).
EMBL: AP180889; AAF78472.1; -.
ZFIN; ZDB-GENE-000322-3; tnnt.
InterPro; IPR001978; Troponin.
Pfam; PF00992; Troponin; 1.
                             MEDLINE-93054628; PubMed-1429653;
Pan B.S., Potter J.D.;
"Two genetically expressed troponin T fragments beta isoforms exhibit functional differences.";
J. Biol. Chem. 267:23952-23056(1992).
InterPro; IPR001978; Troponin.
Pfam; PF00992; Troponin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Troponin T alpha isoform.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                     Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
First skeletal muscle troponin T.
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01-OCT-2000
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       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ERAEQQRLKSQ 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Troponin; 1.
AA; 27786 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68
27809 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66.1%;
63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.1%;
63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41; DB
Pred. No. 18;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
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Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
1AF4A69100C5A97A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37729A66290252DD CRC64;
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18;
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ERAEQORLKSO 11

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RESULT
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Q9TS31
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Ouery Match
Best Local S
Matches 7
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Matches
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Best Local S
Matches 7
                                                                                                                                        TISSUE-HEART MUSCLE;
MEDLINE-9612958; PubMed-8576938;
MEDLINE-9612958; PubMed-8576938;
Townsend P.J. Barton P.J.R., Yacoub M.H., Far
Twomsend P.J. Barton P.J.R., Yacoub M.H., Far
"Molecular cloning of human cardiac trponin T
developing and failing heart.";
J. Mol. Cell. Cardiol. 27:223-2236(1995).
EMBL; X79861; CAA56240.1;
EMBL; X79861; CAA56240.1;
InterPro; IPRO001978; Troponin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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O9TS31;

O1-MAY-2000 (TrEMBLrel. 13, C
01-MAY-2000 (TrEMBLrel. 13, L
01-JUN-2001 (TrEMBLrel. 17, L
                                                                                                                                                                                                                                                                                                                                                                                              015607 PRELLAR....
015607; O15607; O15607; O1FEMBLrel. 01, Created)
01-NOV-1996 (TREMBLrel. 01, Last sequence update)
01-DEC-2001 (TREMBLrel. 19, Last annotation update)
01-DEC-2001 (TremBLrel.).
                                                                                   NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cardiac troponin T (Fragment)
Homo Sapiens (Human)
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Two genetically expressed troponin T fragments representing alpha and beta isoforms exhibit functional differences.";
J. Biol. Chem. 267:23052-23056(1992).
InterPro: IPR001978; Troponin.
Pfam; PF00992; Troponin; 1.
SEQUENCE 249 AA; 29683 MW; ABEAA7AC4E86FCCF CRC64;
                                                                                                                               Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-93054628;
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pan B.S., Potter J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12
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                                                                                                       PF00992; Troponin; 1.
ER 250 250
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Similarity 63.07; Conservative
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7; Conserv
                                                                                   250 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=1429653
                                                                                   30151 MW;
                     66.1%;
63.6%;
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63.6%;
  ..
                     Score 41;
Pred. No.
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Last sequence up
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Pred. No. 18;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                          Yacoub M.H., Farza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                   975F687EB21B33D6 CRC64;
  Mismatches
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19;
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  Indels
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ERAEQQRIRNE 138

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RESULT
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Best Local
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Q95MC6;
Q05MC6;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Troponin T splicing mutant isoform 2.
Troponin T splicing motant isoform 2.
Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               090247 PRELIMINARY; PRT; 271 AA.
090247; Q90246; 035575; 035576; 035577; 035581; 035581; 035581; 035581; 035581; 035581; 035582; 035583; 035584; 035884; 035885; P97456;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Troponin T, fast skeletal muscle isoforms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cardiomyopathy.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AY005143; AAG23718.1; -.
InterPro; IPR001978; Troponin.
Pfam; PF00992; Troponin; 1.
SEQUENCE 270 AA; 32339 MW; 316105372CACC80D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING. STRAIN—129/SVU; TISSUE—SKELETAL MUSCLE; MEDLINE—97390134; Pubmed—9249073; Wang J., Jin J.-P.; Wang J., Jin J.-P.; Trimary structure and developmental acidic to the structure acidic to the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis. NCBI_TaxID=9615;
                                                                                                             MARRIM. GENOME 8:346-348(1997).

- FUNCTION: TROPONIN T IS THE TROPOMYOSIN-BINDING SUBUNIT OF TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS CALCIUM-SENSITIVITY TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIONAL
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM B3E17).
MEDLINE-97262102; PubMed-9107680;
KOCh A., Juan T.S.-C., Jenkins N.A.,
McNiece I.K., Fletcher F.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Primary structure and developmental acidic to basic transition alternatively spliced mouse fast skeletal muscle troponin T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TNNT3
                                                                                                                                                                                                                             troponin
                                                                                                                                                                                                                                                                                                                                                                                                                         Gene 193:105-114(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Dog cardiac troponin T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           isoforms
                                                                                                                                                                                                                             cDNA cloning and chromosomal mapping of
croponin T.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 ERAEQQRIRNE 126
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(BY SIMILARITY).
ALTERNATIVE PRODUCTS: AT LEAST 13 ISOFORMS; Ale17 (SHOWN HERE), A2E17, A3E17, A4E17, A5E17, A6E17, B1E16, B2E17, B2E16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 63.7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11
                                                                                                                                                                                                                                                                                                                                                            (ISOFORM B3E17).
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63.6%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       variants relating
                                                                                                                                                                                                                                                                                                           Gilbert D.J.,
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                                                                                                                                                                                                                                                          fast skeletal muscle
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                                                                                                                                                                                                                                                                                                              Copeland N.G.,
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                                                                                                                ACTIVITY
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Search completed: March 13, Job time: 28.9455 secs

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                                                                 Query Match
Best Local s
Matches 7
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-!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN SKELETAL MUSCLE.
-!- DEVELOPMENTAL STAGE: EMBYO AND NEONATE EXPRESS PREDOMINANTLY ACIDIC ISOFORMS WHILE ALL ADULT ISOFORMS ARE BASIC. ONLY ONE ISOFORM, B2E17, IS FOUND IN BOTH EMBRYO/NEONATE AND ADULT. A TRANSITION FROM HIGH TO LOW MOLECULAR WEIGHT ISOFORMS IS ALSO SEEN DURING POSTMATAL LEVELOPMENT.

EMBL; L49466; AAB67290.1; -- EMBL; L49467; AAB67290.1; -- EMBL; L49472; AAB67291.1; -- EMBL; L49472; AAB67291.1; -- EMBL; L49472; AAB67293.1; -- EMBL; L4999; AAB67283.1; -- EMBL; L4899; AAB67283.1; -- EMBL; L4899; AAB67283.1; -- EMBL; L4899; AAB67287.1; -- EMBL; L4891; AAB67287.1; -- EMBL; L4893; AAB67287.1; -- EMBL; L4891; -- EMBL; L4891; AAB67287.1; -- EMBL; L4891; AAB67288.1; -- EMBL;
                                                                                                                                       CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOD_RES
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phosphorylation.
INIT_MET 0
MOD_RES 1
VARSPLIC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
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EMBL;
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Pfam; PF00992; Troponin; 1.
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115
                                1 ERAEQQRLKSQ 11
ERAEQQRIRAE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein; Alternative
                                                                   Similarity 7; Conser
                                                                                                                                   251
271
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                                                                                                                                                                                                                                                                 242
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                                                                                                                                         ₹:
                                                                                                                                                                                      AND ISOFORM B3E16).

MISSING (IN ISOFORM A5E17, ISOFORM A6E17
ISOFORM B2E17 AND ISOFORM B2E16).

TILRERIDOAQKH -> MTVRARVEMLAKF (IN ISOFORM B1E16, ISOFORM B2E16, ISOFORM B3E16 AND ISOFORM B4E16).

P -> R (IN AAB67283, AAB67284, AAB67285, AAB67286, AAB67287, AAB67288 AND
                                                                 Score 41; DB
Pred. No. 21;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  splicing; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                      B4E16)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHORYLATION (BY CK2) (BY SIMILARITY).
MISSING (IN ISOFORM A4E17, ISOFORM B3E17,
ISOFORM B3E16, ISOFORM B4E17 AND ISOFORM
                                                                                                                                                       Þ
                                                                                                                                                                                                                                                                                                                                   AND ISOFORM MISSING (IN
                                                                                                                                                                                                                                                                                                                                                                                                       AND ISOFORM B2E16).
MISSING (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                                                         MISSING
                                                                                                                                                                                                                                                                                                                                                                                                                                           MISSING (IN ISOFORM A3E17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             B4E16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
                                                                                                                                                                           AAB67289).
                                                                                                                                     -> T (IN REF. 2).
D2CBB544B8C7953F
                                                                                                                                                                                                                                                                                                                                                                      (IN ISOFORM A2E17,
                                                                                                      DB 11;
                                                                                                                                                                                                                                                                                                                                                   A6E17).
                                                                                                                                                                                                                                                                                                                                   ISOFORM BIE16,
                                                                   0;
                                                                                                  Length 271;
                                                                                                                                         CRC64;
                                                                                                                                                                                          , AAB67284, AAB67285
AAB67288 AND
                                                                                                                                                                                                                                                                                                                                                                                                        B4E17 AND ISOFORM
                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                      ISOFORM A4E17
                                                                                                                                                                                                                                                                                                                                                                                                                                           ISOFORM B2E17
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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62
1 ERAEQQRLKSODL
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Gapop 10.0 , Gapext 0.5
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    SwissProt_40:*
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    BB
TRT3_COTJA
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CAFA_MOUSE
CAFA_HUMAN
TRN1_XENLA
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P02642 gallus gall
P06398 coturnix co
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P13789
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8 streptococc
5 homo sapien
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manduca sex
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ific an	Kishimoto	ALTERNATIVE SPLICING. MEDLINE-89028672; Publ	286:81	K.U., Magnenat l characterizat	38513;	.114	d expre	Hofstet	OM N.A. 18454;	-665(19	., Saki	, Inui	OM N.A. 51737;	Acad.	hocyte with a	akami M Yodoi J	OM N.A.	9606;	ens (Human) ; Metazoa; Futberia:	EBF.	FC-epsi	(Rel.	(Rel.			54.8 54.8	44	6.	6.	.0.0	, o
numan FC e and IL-4-s 1988)	oto ii	E SPLICING. 028672; PubMed=2	9-824(19	enat E., Aubonne rization of natu	PubMed	1987).	ssion	ter H.	PubMed.	86).	yama F., S	S., Sat	PubMed•	Sci. U	ocyte Fc recepto with animal lect	., Kim	PubMed•	, F 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	n). Chore		lon-RI	06, Las	06, Cre	STANDARD;		413 416 506	349 388	1790	732	652	590
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cific		2386;	·	Aubonney I	7742;		he cDN	., Sarfati M. Delespesse G	4567;		, Suemura M., uman lymphocyt	havash	7743;	84	r for ins.";	., Hon	932	6	; Cran		epsilo	equenc	<u>o</u>	PRT;	ALI	FL1_TOBAC FL2_TOBAC Y213_MYCPN	DIA2_M PAM_ST	SEPA_E	CADL_C	DREB_C	HMAA_D
regulation of ge		Oato D Baroumian		N., Bonnefoy JY.	Pochon S. Regames		coding for a	M., Levy C.A., Su			M., Kishimoto T.	n E.L., Owa		819-823(1987).	gE: sequence	jo T., Miyoshi T.		ttittit, monthiton	iata; Vertebrata;		(BLAST-2) (Immuno	Rel. 06, Last sequence update) Rel. 41, Last annotation update)		321 AA.	TS.)BAC)BAC IYCPN	RPY	MENI	HICK	HICK	ROME
ne expressi		ਲ ਹ		human s	5		human lymphocyte	ter U., ł			ñ.,	Hirano T			homology of i	, Tagaya Y			Euteleost						•	Q40504 Q40505 P75478	56	21	350	22	55
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PIR; /
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein Sci. 5:240-247(1996).

- FUNCTION: THIS RECEPTOR HAS ESSENTIAL ROLES IN THE RE-
OF IGE PRODUCTION AND IN THE DIFFERENTIATION OF B-CEL
A B-CELL-SPECIFIC ANTIGEN).

- 1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Padlan E.A., Helm B.A.;
"Modeling of the lectin-homology
affinity Fc epsilon receptor (Fc
Receptor 3:325-341(1993).
[7]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bajorath J., Aruffo A.;
"Structure-based modeling of the ligand binding of the ligand binding of two cell surface receptor CD23 and comparison of two deals of the ligand binding of two cells are receptor."
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3D-STRUCTURE MODELING
MEDLINE=94191542; Publ
                                                                                                                                                                                                                                                                                                         PDB; 1HLI; 31-JAN-94.
PDB; 1KJE; 03-APR-96.
                                                                  REPEAT
                                                                                                                                  TRANSMEN
                                                                                                                                                 DOMAIN
                                                                                                                                                              CHAIN
                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                        Pfam; PF00059; lectin_c; SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                            Genew; HGNC:3612; FCER2
                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             derived molecular models.";
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                                                                                                                                                                                       Repeat;
                                                                                                                                                                                                  ge-binding
                                                                                                                                                                                                                              PROSITE;
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InterPro; IPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3D-STRUCTURE
                                                                                                                                                                                                                                                                                                                               3L; M15059; AAA52434.1; -.
8L; M04766; AAA52435.1; -.
8L; M04772; CAA28465.1; -.
8L; M23562; AAA52433.1; -.
8; A26067; LNHUER.
8; A26164; A26164.
8; A26589; A26589.
8; A31924; A31924.
8; JL0132; JL0132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A SOLUBLE EXCRETED FORM.

A SOLUBLE PROBLET FORM.

AND O-GLYCOSYLATED.

MISCELLARBOUS: THERE ARE TWO KINDS OF FC RECEPTORS FOR IGE, WHICH DIFFER IN BOTH STRUCTURE AND FUNCTION: HIGH AFFINITY RECEPTORS ON DIFFER IN BOTH STRUCTURE AND LOW AFFINITY RECEPTORS ON LYMPHOCYTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN. DATABASE: NAME=PROW; NOTE=CD guide CD23 entry; WMW="http://www.ncbi.nlm.nlh.gov/prow/cd/cd23.htm".
                                                                                                                                                                                       Lectin;
                                                                                                                                                                                                            PS00615; C_TYPE_LECTIN_1; 1. PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                 IPR001304; Lectin_C.
 48
162
149
69
90
111
160
163
                                                                                                                                                                                                    protein;
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                                                                                                                                                                        Signal-anchor; Alternative splicing; 321 MEMBRANE BOUND FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LING OF LECTIN DOMAIN. Pubmed-8142907;
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 321
284
150
150
110
111
131
131
288
174
                                                                                                                                                                                    Transmembrane; Glycoprotein; Receptor; B-cell; al-anchor; Alternative splicing; 3D-structure.
                                                                                                                           SOLUBLE FORM.
CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (TYPE-II MEMBRANE
             BY
BY
                                                                             (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
C-TYPE LECTIN (LONG FORM)
CLEAVAGE.
             SIMILARITY
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epsilon
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OF B-CELLS (IT I
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Muscle protect
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CARBOHYD
VARSPLIC
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                           and skeletal muscle development.*;
Science 226:979-982(1984).
-!- FUNCTION: TROPONIN T IS THE TROPOMYOSIN-BINDING SUBUNIT O
TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONF
CALCIUM-SENSITIVITY TO STRIATED MUSCLE ACTOMYOSIN ATPASE
-!- ALTERNATIVE PRODUCTS: 2 isoforms; 1/Embryonic form (shown and 2/Adult form; are produced by alternative splicing.
-!- SIMILARITY: BELONGS TO THE TROPONIN T FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
01-AUG-1988 (Rel. 08, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Troponin T, cardiac muscle isoforms (Tollies gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata
                                       SEQUENCE
                                                                                                                                                        EMBL; M10013; AAA49099.1;
EMBL; K02263; AAA49098.1;
PIR; A03086; TPCHTC.
PIR; A25373; A25373.
                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-85065747; PubMed-6095446; Cooper T.A., Ordahl C.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "A single cardiac troponin T gene generates embryonic and adult isoforms via developmentally regulated alternate splicing."; J. Biol. Chem. 260:11140-11148(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORMS 1 AND MEDLINE-85289327; PubMed-2993302; Cooper T.A., Ordahl C.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHICK
                                                   VARSPLIC
                                                                                                                  Pfam; PF00992; Troponin; 1.
Muscle protein; Alternative
                                                                                                                                                                                                                         or send an
                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                   Cooper T.A., Ordahl C.P.;
"A single troponin T gene regulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P02642;
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                                                                                                                                           InterPro; IPR001978; Troponin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 67-301 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archosauria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9031;
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321 AA;
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E
                                                                                                                  splicing; Multigene family;
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MEEGQYS -> MNPPSQ (IN ISOFORM B).
N -> T (IN REF. 3).
          Score
                                                  BY SIMILARITY.
PHOSPHORYLATION (BY CK2)
(BY SIMILARITY).
MISSING (IN ISOFORM 2).
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Pred. No.
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                                       F85CE1A47F07DD94 CRC64
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Best Local Similarity

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Best Local :
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Muscle proc...
Phosphorylation.
OTTT_MET
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J. Biol.
                                                                            VARSPLIC
VARSPLIC
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                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no use by non-profit institutions as long as its con modified and this statement is not removed. Usage b
                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-86033836; PubMed-3840482;
Hastlings K.E.M., Bucher E.A., Emers
"Generation of troponin T isoforms
avian skeletal muscle. Conserved an
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINE-89308680; PubMed*2745456;

MEDLINE-89308680; PubMed*2745456;

Bucher E.A., de la Brousse F.C., Emerson C.P. Jr.;

"Developmental and muscle-specific regulation of an troponin T isoform expression by mRNA splicing.";

J. Biol. Chem. 264:12482-12491(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRT3
                                                         SEQUENCE
                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coturnix coturnix japonica (Japanese quail).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
                                                                                                                                                                                                                                                                                           This
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                                                                                                                                  Muscle protein; Alternative splicing; Multigene family;
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                                                                                                                                                                                                                                                                                                           ALTERNATIVE PRODUCTS: AT LEAST THREE ISOFORMS ALTERNATIVE SPLICING.
SIMILARITY: BELONGS TO THE TROPONIN T FAMILY.
                                                                                                                                                                                                                                                                                                                                       3101. Chem. 260:13699-13703(1985).
FUNCTION: TROPONIN T IS THE TROPONYOSIN-BINDING SUBUNIT OF
TROPONIN. THE THIM FILAMENT REGULATORY COMPLEX WHICH CONFERS
CALCIUM-SENSITIVITY TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.
                                                                                                                                                               A03085; TPQJT2.
A03084; TPQJT1.
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M26599;
M11685;
M11684;
                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the E
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 ERAEQORLKSO 11
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                                                                                                                                              PF00992; Troponin;
                  7; Conserv
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                                                                                                                                                    IPR001978; Troponin.
                                                         252
                    Conservative
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225
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forms by alternative
ved and divergent fea
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TRT3_HUMAN
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P45378;
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TRT3_RAT 9
P09739; P09740;
01-MAR-1989 (Rel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPUTATION (Human).
Homo sapiens (Human).
Tharvota; Metazoa; Chordata; Metazoa; Primates;
                                                                                                                                                                                                                                                                                                         Muscle protein; Multigene family; Phosphorylation.
INIT_MET 0 0 BY SIMILARITY.
MOD_RES 1 1 PHOSPHORYLATION (BY C
                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M21984; AAA36777.1; -
EMBL; AF026276; AAF21629.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Isolation and characterization of human T cDNA: comparative sequence analysis of the evolution of members of a multigene f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Troponin T, fast skeletal muscle isoform beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Cell Biol.
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MEDLINE-94226695; PubMed-8172653;
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nes 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                    HGNC:11950; TNNT3.
                                                                                                                                                                                                                                                                                                                                                                              IPR001978; Troponin.
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 (Rel. 10, Created)
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Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M.K.,
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                                     258
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                                                                                                                                                                                                                                       Length 257;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Intricate combinatorial patterns of exon splicing generate multiple regulated troponin T isoforms from a single gene.";

Cell 41:67-82(1985),

-1- FUNCTION: TROPONIN T IS THE TROPOMYOSIN-BINDING SUBUNIT OF TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS CALCIUM-SENSITIVITY TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.

-1- ALTERNATIVE PRODUCTS: AT LEAST 44 ISOFORMS ARE PRODUCED BY ALTERNATIVE SPLICING. THE ALPHA AND BETA FORMS ARE PRODUCED BY THE USE OF MUTUALLY EXCLUSIVE EXONS.

1- SIMILARITY: BELONGS TO THE TROPONIN T FAMILY.
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15-JUN-2002
                EMBL, 
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Breitbart R.E., Nadal-Ginard B.;
"Complete nucleotide sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nadal-Ginard B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE-85201690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alternatively spliced exons divergence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-86281691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                             M15202: AAA96446.1;

M15202: AAA96464.1;

M15202: AAA96454.1;

M15202: AAA96456.1;

M15202: AAA96456.1;

M15202: AAA96467.1;

M15202: AAA9647.1;

M15202: AAA9647.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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AAA9644711

AAA9644711
 AAA96449.
AAA964440.
AAA964483.
AAA964483.
AAA96449.
AAA96460.
AAA96462.
AAA96451.
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guyen H.T., Medford
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Last annotation updat
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; Murinae; Rat
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TRT3_CHICK
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Best Local S
Matches 7
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SEQUENCE FROM N.A.
MEDLINE-89066672; PubMed-3198600;
Smillie L.B., Golosinska K., Rein-
"Sequences of complete cDNAs enco
"Sequence" of transporter T.";
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                 This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an
                                                                                                                                                                    Skeletal muscle troponin T.".

J. Biol. Chem. 263:18816-18820(1988).

-:- FUNCTION: TROPONIN TIS THE TROPOMYOSIN-BINDING SUBUNIT OF TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS CALCIUM-SENSITIVITY TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.

-!- ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS; TNT-1, TNT-2, TNT-3 (SHOWN HERE) AND TNT-4; ARE PRODUCED BY ALTERNATIVE SPLICING.

-!- SIMILARITY: BELONGS TO THE TROPONIN T FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRT3_CHICK STANDARD; PRT; 262 AA.
P12620; P12621; P12619; P12618;
01-OCT-1989 (Rel. 12, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Troponin T, fast skeletal muscle isoforms.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves; Neognathae; Galliformes; Phasiani
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INIT_MET 0
MOD_RES 1
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M15202; AAA96465.1; -...

L; M15202; AAA96470.1; -...

L; M15202; AAA96470.1; -...

L; M15202; AAA96472.1; -...

L; M15202; AAA96472.1; -...

L; M15202; AAA96477.1; -...

L; M15202; AAA96477.1; -...

L; M15202; AAA96477.1; -...

L; M15202; AAA96470.1; -...

L; M15202; AAA96470.1; -...

L; M15202; AAA96480.1; -...

L; M15202; AAA96480
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  license agreement (See license@isb-sib.ch).
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63.68;
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(BY SIMILARITY).

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encoding four
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37BDD772A4F28C7E CRC64;
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EMBL; M22158; AAA49101.1; -.
EMBL; M22155; AAA49101.1; -.
EMBL; M22154; AAA49100.1; -.
PIR; A31957; A31957.
PIR; B31957; B31957.
PIR; C31957; B31957.
PIR; C31957; B31957.
PIR; C31957; D31957.
PIR; D31957; D31957.
PIR; D31957; D31957.
PIR; D31957; D31957.
               SEQUENCE OF 1-66 FROM N.A., AND ALTERNATIVE SPLICING.
STRAIN-New Zealand white; TISSUE-Skeletal muscle;
MEDLINE-90323375; pubMed-2373251;
Briggs M.M., McGinnis H.D., Schachat F.;
"Transitions from fetal to fast troponin T isoforms are coordinated with changes in tropomyosin and alpha-actinin isoforms in developing rabbit skeletal muscle.";
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-10; 17-43 AND 56-278.

MEDLINE-77118575; PubMed-320204;

Pearlstone J.R., Johnson P., Carpenter M.R., Sn

"Primary structure of rabbit skeletal muscle tr

determination of the NH2-terminal fragment CB3

sequence of troponio-T.",

Biol. Chem. 252:983-989(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P02641; P19349; P19350;
21-JUL-1986 (Rel. 01, Created)
01-OCT-1996 (Rel. 34, Last sequence update
15-JUN-2002 (Rel. 41, Last annotation updat
Troponin T, fast skeletal muscle isoforms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARSPLIC
VARSPLIC
                                                                                                                                                                                        Briggs M.M., Schachat F.;
"Origin of fetal troponin T: developmentally new exon in the fast troponin T gene.";
Dev. Biol. 158:503-509(1993).
                                                                                                                                                                                                                                                                              [2]
SEQUENCE OF 1-66 FROM N.A., AND ALTERNATI'STRAIN-New Zealand white; TISSUE-Skeletal MEDLINE-93345743; PubMed-8344466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
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INIT_MET 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF00992; Troponin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein; Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        262 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cuniculus (Rabbit)
Metazoa; Chordata; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38
235
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247
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63.6%;
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ne family;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1).
MISSING
TNT-4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION (BY CK2)
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                       ALTERNATIVE SPLICING E=Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leporidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alternative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
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troponin-T. S
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                                                                                                                                                                                                                                                                                                                                                                                                                  and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 262;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                  EMBL; U04970; AAA16023.1; --
EMBL; U04971; AAA16025.1; --
EMBL; U04972; AAA16026.1; --
EMBL; U04973; AAA16027.1; --
EMBL; U04974; AAA16027.1; --
EMBL; U04975; AAA16028.1; --
EMBL; U04975; AAA16029.1; --
EMBL; U04976; AAA16030.1; --
EMBL; U04977; AAA16030.1; --
EMBL; U04978; AAA16031.1; --
EMBL; U04978; AAA16031.1; --
FIR; R03083; TPRBTS.
PIR; S03590; S03590.
PIR; S03591; S03591.
PIR; S03592; S03592.
PIR; S03592; S03593.
             CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Briggs M.M., Schachat F.;
"N-terminal amino acid sequences
troponin T isoforms from rabbit:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-New Zealand white;
Briggs M.M., Schachat F.;
                                                                                                                                                                                                                                                                                                     MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001978; Troponin. Pfam; PF00992; Troponin; 1. Muscle protein; Multigene fami
                                                                                                                                                 VARSPLIC
                                                                                                                                                                                          VARSPLIC
                                                                                                                                                                                                                                     VARSPLIC
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                                                                                                                                                                                                                                                                                                                                              INIT_MET
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                                                                                                                                                                                                                                                                                                                                                                                                                             interPro;
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35
61
278
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ol. 206:245-249(1989).
                                                                                                                                                                                                                                                                                                                                                                    splicing
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36
61
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                  ž
                                                                                                                                                                                                                                                                                                                                                                                         family; Phosphorylation;
                                                      MISSING (IN ISOFORM TNT3, IS
AND ISOFORM TNT4F).
MISSING (IN ISOFORM TNT2, IS
AND ISOFORM TNT2.5F).
MISSING (IN ISOFORM TNT1F, I
MISSING (IN ISOFORM TNT1F, I
SOFORM TNT2PA, ISOFORM TNT1
TNT3F AND ISOFORM TNT4F).
Q -> E (IN REF. 1).
VH -> HV (IN REF. 1 AND 5).
                                      MISSING
                                                                                                                                                                                                                                                     PHOSPHORYLATION (BY MISSING (IN ISOFORM TNT2.5F AND ISOFORM
                                                                                                                                                                                                                                                                                                                            ACETYLATION
                  3D5A7E5F661E4CA9
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E (IN NEF. 1 A)

TNT2

.5F,

ISOFORM

ISOFORM TNT2F

ISOFORM TNT2FA ISOFORM

TNT3F

CRC64;

ISOFORM ISOFORM ISOFORM ITOTAF).

TNT2F,

ISOFORM

Acetylation;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-77157104; PubMed-849266;
Moir A.J.G., Cole H.A., Perry S.V.;
Moir Parry S.V.;
The phosphorylation sites of troponin T from and the effects of interaction with troponin C phosphorylation by phosphorylase kinase.";
Biochem. J. 161:371-382(1977),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-43 AND 56-65.
STRAIN=New Zealand white; TISSUE-Skeletal muscle;
MEDLINE-89199646; PubMed-2704041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [4] SEQUENCE OF 1-66 FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: TROPONIN T IS THE TROPOMYOSIN-BINDING SUBUNIT OF TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS CALCIUM-SENSITIVITY TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY. ALITERNATIVE PRODUCTS: 9 ISOFORMS; TNT1 (SHOWN HERE), TNT1F, TNT2, TNT2F, TNT2FA, TNT2.5F, TNT3F AND TNT4F; ARE PRODUCED BY ALITERNATIVE SPLICING.

PIM: SER-168 OR SER-169 AND SER-175 OR SER-176 ARE PHOSPHORYLATED PIM: SER-168 OR SER-169 AND SER-175 OR SER-176 ARE PHOSPHORYLATED
                                                                                                                                                                                                                                                                                                       IN VITRO BY PHOSPHORYLASE KINASE. SIMILARITY: BELONGS TO THE TROPONIN T FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AND ALTERNATIVE SPLICING
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RESULT 8
TRT2_BOVIN
ID TRT2_B
AC P13789
DT 01-DEC
DT 15-JUN
RA LESZYK
RA LES
 TRT2_SHEEP
ID TRT2_S
AC P50751
DT 01-OCT
DT 01-OCT
                                                                                       RESULT
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TRTZ_BOVIN
TRTZ_BOVIN
P13789; p13790;
f 01-JAN-1990 (Rel. 13, Created)
f 15-DEC-1998 (Rel. 37, Last sequence update)
JT 15-DUN-2002 (Rel. 41, Last annotation update)
Troponin T, cardiac muscle isoforms (TnTC).
                                                                                                                                                                                                               Query Match
Best Local S
Matches 7
 TRT2_SHEEP
P50751;
01-OCT-1996
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Noland T.A. Jr., Raynor R.L., Kuo J.F.;

"Identification of sites phosphorylated in bovine cardiac troponin I and troponin T by protein kinase C and comparative substrate activity of synthetic peptides containing the phosphorylation sites.";

J. Biol. Chem. 264:20778-20785(1989).

-I- FUNCTION: TROPONIN T IS THE TROPOMYOSIN-BINDING SUBUNIT OF TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS CALCIUM-SENSITIVITY TO STRIATED MUSCLE ACTOMYOSIN APPASE ACTIVITY.

-I- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are produced by alternative splicing.

-I- SIMILARITY: BELONGS TO THE TROPONIN T FAMILY.

PIR; A28008; A28008.
                                                                                                                                                                                                                                                                                                   MOD_RES
MOD_RES
MOD_RES
VARSPLIC
                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-88107637; PubMed-3122824;
Leszyk J., Dumaswala R., Potter J.D.,
Tobacman L.S., Collins J.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
NCBI_TaxID-9913;
                                                                                                                                                                                                                                                                                                                                                                                          MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-90062225; PubMed-2584239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochemistry 26:7035-7042(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                            Muscle
                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001978; Troponin.
Pfam; Pr00992; Troponin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                   Similarity 63. 7; Conservative
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199
280
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284
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                                                      STANDARD;
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199
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                                                                                                                                                                                                                                                                                    33782 MW;
                                                                                                                                                                                                                                   66.1%;
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63.6%;
Created)
Last sequence update)
                                                                                                                                                                                                                               .68;
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                                                                                                                                                                                                                              Score 41;
Pred. No.
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AAEEEH -> N (IN ISC)
0B7F3A59A5138530
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Pred.
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                                                    PRT;
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(BY PKC).
ISOFORM 2).
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                                                                                                                                                                                                                                              Length 284;
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TRT2_HUMAN
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Best Local S
Matches 7
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Mammalia; Eutheria; (
Bovidae; Caprinae; Ov
NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRT2_HUMAN STANDARD; PRT; 297 AA P45379; Q99596; Q99597; O60214; O1-NOV-1995 (Rel. 32, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation updat Troponin T, cardiac muscle isoforms (TnTC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pediatr. Res. 29:580-585(1991).

1- FUNCTION: TROPONIN T IS THE TROPOMYOSIN-BINDING SUBUNIT OF TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONVERS CALCIUM-SENSITIVITY TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.

1- DEVELOPMENTAL STAGE: EXPRESSED FROM MIDGESTATION TO ADULT LIFE.

1- SIMILARITY: BELONGS TO THE TROPONIN T FAMILY.

INTERPROL 178001978; Troponin.
MEDLINE=96129582;
                                                               assignment of the TNNT2 to
Genomics 21:311-316(1994).
                                                                                                                      Townsend P.J., Farza H., Macgeoch C., Gahlman R., Yacoub M.H., Barton P.J.R.
                                                                                                                                                                            TISSUE-Heart
                                                                                                                                                                                                                                                                                 Mesnard L., Samson Mercadier J.-J.;
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
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Eukaryota; Metazoa; C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Fetal heart;
MEDLINE-91326551; PubMed-1866215;
MCAulliffe J.J., Robbins J.;
"Troponin T expression in normal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-2002 (Rel. 41, Last annotation update) Troponin T, cardiac muscle isoform (TnTC).
                                  SEQUENCE FROM N.A.
                                                                                 "Human cardiac troponin T: identification of fetal assignment of the TNNT2 locus to chromosome 1q.";
                                                                                                                                                        TISSUE-Heart muscle;
MEDLINE-94375053; PubMed-8088824;
                                                                                                                                                                                                                                              troponin T.
                                                                                                                                                                                                                                                                                                                   MEDLINE-93345675; PubMed-8344420;
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                                                                                                                                                                                                                                                  "Molecular cloning
troponin T.";
                                                                                                                                                                                                                                                                                                                                       rissue-Heart;
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Primates;
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Erdmann J.,
Fleck E., Re
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  developing and failing heart.";
J. Mol. Cell. Cardiol. 27:2223-2236(1995).
[4]
                                                                                             MEDLINE-95206332; PubMed-7898523; Watkins H., McKenna W.J., Thierfelder L., O'Donoghue A., Spirito P., Matsumori A.,
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D'Cruz L.G.
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                                                                                                                                                                  Thierfelder L., Watkins H., Macrae C., Lamas R., Vosberg H.-P., Seidman J.G., Seidman C.E.; "Alpha-tropomyosin and cardiac troponin T mutatic hypertrophic cardiomyopathy: a disease of the sar
                                                                                                                                                                                                                                                     "The major protein expression profile and database of human heart."; Electrophoresis 16:1160-1169(1995).
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Kovalyov L.I., Shishkin S.S., Efimochkin A.S.,
Ershova E.S., Egorov T.A., Musalyamov A.K.;
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"A rapid protocol for cardiac troponin',
familial hypertrophic cardiomyopathy.";
Hum. Mutat. 11:179-182(1998).
                                             "Mutations in the genes for cardiac c
in hypertrophic cardiomyopathy.";
New Engl. J. Med. 332:1058-1064(1995)
                                                                                                                                                                                                                                                                                                                                                            Submitted (FEB-1997) to
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Regitz-Zagrosek V.;
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                PRO-287.
Wischke S.,
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Moravec C.
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hypertrophic cardiomyopathy without left '
InterPro; IPR001978; Tropenin;
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7 and 8 are expressed in fetal heart. Isoform 7 is also expressed in failing adult heart.

DISEASE: DEFECTS IN TUNT2 ARE ONE OF THE CAUSES OF FAMILIAL HYPERTROPHIC CARDIOMYOPATHY (FHC) WHICH IS AN AUTOSOMAL DOMINANT DISORDER CHARACTERIZED BY INCREASED MYOCARDIAL MASS WITH MYOCYTE AND MYOFIBRILLAR DISARRAY. THIS FORM OF FHC IS KNOWN AS CMH2.

IT IS A DISEASE OF THE SARCOMERE.

IT IS A DISEASE OF THE SARCOMERE.
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Pro
                                                                                                                                                                                                                                               AF004415; AAC39590.1

AF004416; AAC39590.1

AF004418; AAC39590.1

AF004419; AAC39590.1

AF004419; AAC39590.1

AF004420; AAC39590.1

AF004421; AAC39590.1

AF004421; AAC39590.1

AF004421; AAC39590.1

AF004421; AAC39590.1

AF014213; AAC39597.1;

AF01124; AAC39597.1;

AF01124; AAC39597.1;
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X74819; CAA52818.1;
L40162; AAA67422.1;
X79855; CAA56235.1;
X79856; CAA56237.1;
X79857; CAA56237.1;
X79858; CAA56238.1;
X79858; CAA70841.1;
Y99627; CAA70841.1;
Y99628; CAA70841.1;
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nian C., Davison
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE=93059379; PubMed=1433301;

MIN J.-P., Huang O.O., Yeh H.I., Lin J.J.C.;

"Complete nucleotide sequence and structural organization of cardiac troponin T gene. A single gene generates embryonic an cardiac troponin T. Sene. A single gene generates embryonic and the sequence of the sequence o
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                                                                                                                       s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restr
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R -> L (IN FHC CMH2).
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ID TRT2_MA
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DT 15-JUN
DE Tropon
GN Tropon
GN TRNICA
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OC HARMMAIL
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01-0CT-1996 (Rel. 34, Last sequence upo
01-0CT-1996 (Rel. 34, Last annotation
15-JUN-2002 (Rel. 41, Last annotation
Troponin T, cardiac muscle isoforms (T
                                                                VARSPLIC
VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YOphon.
TNNT2.
Mus musculus (Mouse).
Mus musculus (Mouse).
Metazoa; Chordata; Metazoa; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARSPLIC CONFLICT
                                                                                                                                                                                                                                                                                   EMBL; L47553; AAA85349.1;
EMBL; L47600; AAA85352.1;
MGD; MGI:104597; Tnnt2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jin J.-P., Wang J., Zhang J.;
Submitted (JAN-1996) to the EmbL/GenBank/DDBJ databases.

1- FUNCTION: TROPONIN T IS THE TROPOMYOSIN-BINDING SUBUNIT OF
TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS
CALCIUM-SENSITIVITY TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.

1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; EMBRYONIC/EA (SHOWN HERE) AND
A3B; ARE PRODUCED BY ALTERNATIVE SPLICING.
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INIT_MET 0
MOD_RES 1
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INIT_MET 0
MOD_RES 1
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Pfam; PF00992; Troponin; 1.
Muscle protein; Alternative splicing; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO THE TROPONIN T FAMILY.
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M26052; AAA42297.1; --
M80829; AAB07676.1; --
                                                                                                                                                                                                                                                 PF00992;
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7; Conserv
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PHOSPHORYLATION (BY
(BY SIMILARITY)
(BY SIMILARITY)
MISSING (IN ISOFORM
MISSING (IN ISOFORM
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W; 3252AEB57E88CE31 (
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Score
Pred.
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Pred. No.
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T -> A (IN REF. 2).
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4.7;
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1.6;
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                    Length 300;
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P09495;
01-MAR-1989
01-MAR-1989
15-JUN-2002
                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                  "Structure and complete nucleotide sequence of the gene encoding rat fibroblast tropomyosin 4.";
J. Mol. Biol. 213:399-405(1990).
-i- FUNCTION: Binds to actin filaments in muscle and nonmuscle cells. Plays a central role, in association with the troponin complex, in the calcium dependent regulation of vertebrate striated muscle contraction. Smooth muscle contraction is regulated by interaction with caldesmon. In nonmuscle cells is implicated in stabilizing cytoskeleton actin filaments.
-i- SUBUNIT: DIMER OF AN ALPHA AND A BETA CHAIN.
-i- DOMAIN: THE MOLECULE IS IN A COILED COIL STRUCTURE. THE SEQUENCE EXHIBITS A PROMINENT SEVEN RESIDUES DERIODICITY.
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MEDLINE-90278950; PubMed-2112608;
Lees-Miller J.P., Yan A., Helfman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yamawaki-Kataoka Y., Helfman D.M.;
"Isolation and characterization of CDNA clones encoding a low molecular weight nonmuscle tropomyosin isoform.";
J. Biol. Chem. 262:10791-10800(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sanotation
15-JUN-2002 (Rel. 41, Last annotation
Tropomyosin alpha 4 chain (Tropomyosin
                                                                                                                                                          Pfam; PF00261; Tropomyosin; 1. PRINTS; PR00194; TROPOMYOSIN; 1. PROSITE; PS00326; TROPOMYOSIN; 1.
                                                                                                                                                                                                                        PIR; A28493; A28493
PIR; S10623; S10623
                                                                                                                                                                                                                                                    EMBL; J02780; AAA42291.1; EMBL; Y00169; CAA68360.1;
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                                                                                                                                Multigene family.
                                                                                                                                                Muscle protein; Cytoskeleton;
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                                                                                                                                                                                                          InterPro;
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145
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4 chain (Tropomyosin 4) (TM-4).
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                                                                    64.5%;
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Pred. No. 5
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MEDLINE-21927593; PubMed-11917108;
Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
"Genome sequence and comparative microarray analysis of serotype M18
group A Streptococcus strains associated with acute rheumatic fever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRPE_STRPY STANDARD; PRT; 1
099YC8; P82581;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2002 (Rel. 40, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
GrpE protein (HSP-70 cofactor).
GRPE OR SPY1761 OR SPYM18_1832.
                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRPY
                                                                                      InterPro; IPR000740; GrpE.
Pfam; PF01025; GrpE; 1.
PRINTS; PR00773; GRPEPROTEIN.
PROSITE; PS01071; GRPE; 1.
Chaperone; Heat shock; Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-MGAS8232 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-SF370 / ATCC 700294 / Serotype MEDLINE-21192684; PubMed-11296296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pyogenes (serotype M18).
Bacteria; Firmicutes; Lactobacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pyogenes, and
                                                                                                                                                                             EMBL; AE010089; AAI HSSP; P09372; 1DKG
                                                                                                                                                                                              EMBL; AE006604; AAK34502.1; -. EMBL; AE010089; AAL98350.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   outbreaks."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAY-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proteins."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Two-dimensional gel electrophoresis map of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /anBogelen R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hogan D.A., Du P., Stevenson T.I., Whitton M., Kilby G.W., Rogers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PARTIAL SEQUENCE, AND MASS SPECTROMETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                 mitted (MAY-2000) to the SWISS-PROT data bank. FUNCTION: STIMULATES, JOINTLY WITH DNAJ, THE ATPASE ACTIVITY OF DNAK. HELPS TO RELEASE ADP FROM DNAK THUS ALLOWING DNAK TO RECY
                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE GRPE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                MORE EFFICIENTLY (BY SIMILARITY).
MASS SPECTROMETRY: MW-22054.54; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Natl. Acad.
                                                                        190
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                                                                        AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sci. U.S.A. 99:4668-4673(2002).
                                                                        22054 MW;
                62.9%;
Score 39; DB 1;
Pred. No. 6.4;
2; Mismatches
                                                                        5636051FC3BAE27E CRC64;
                                                                                        proteome
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                                    Length 190;
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DE Tropon
DE Tropon
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GN Homo s
OC Eukary
OC MAMMAL
RR AGALHAR
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RR 
                                                                                                                      EMBL; M19309; AAA61204.1; -. EMBL; M19308; AAA61205.1; -. EMBL; S69208; AAB30272.1; -. EMBL; S69209; AAB30273.1; -. EMBL; AJ011712; CAA09751.1; -. EMBL; AJ011713; CAA09751.1; JRMBL; AJ011712; CAA09752.1; -. EMBL; AJ011712; CAA09752.1; -. EMBL; AJ011713; CAA09752.1; -. EMBL; AJ01
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MEDLINE-88058976; PubMed-2824479;
MEDLINE-88058976; PubMed-2824479;
Mahan R., Troutt A.B., Wade R.P., Gunning P., Kedes L.;
Gahimann R., Troutt A.B., Gunning P., Kedes L.;
Mahan Silveriates variants in important functional domains of human slow skeletal troponin T.*;
J. Biol. Chem. 262:16122-16126(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-99208666; PubMed-10191089;
Barton P.J.R., Cullen M.E., Townsend P.J., Brand N.J., Mullen A.J.,
Norman D.A.M., Bhavsar P.K., Yacoub M.H.;
"Close physical linkage of human troponin genes: organization,
sequence, and expression of the locus encoding cardiac troponin I and
slow skeletal troponin T.";
Genomics 57:102-109(1999).
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Troponin T, slow skeletal muscle isoforms (Slow troponin T).
TNNT1 OR TNT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restrues by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammaila; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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MEDLINE-94183266; PubMed-8135831;
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Biochem. Biophys. Res. Commun. 199:841-847(1994).
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                                                    interPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: TROPONIN T IS THE TROPOMYOSIN-BINDING SUBUNIT OF TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS CALCIUM-SENSITIVITY TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY. ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2 AND 3; ARE PRODUCED BY ALTERNATIVE SPLICING.
SIMILARITY: BELONGS TO THE TROPONIN T FAMILY.
PF00992; Troponin;
                                            IPR001978; Troponin.
                                                                                                                                                                                                                                                                                                                                                                                                                              ; AAA61204.1; -.
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                                                                                                               Muscle protein; Phosphorylation; Alternative splicing; multigene family.

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AAW13143
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                                                                                                                                    Human soluble CD23
Human soluble CD23
Sequence containin
IgE binding factor
Recombinant Fc_eps
Low affinity Fc_ep
                                 Fc gamma receptor.
Human IgE binding
Sequence encoded b
                                                                                                                                                                                                                                                                                                                                                                                                    Description
Human lymphocyte
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37	38	38	3 8	38	38	38	38	38	38	39	39	39	39	39	39	39	39	41	41	41	41	41	41	41	41	41	41	41	41	53	57	57	57	57
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ALIGNMENTS

RESULT 1 AAW13146

AAW13146;

AAW13146 standard; Protein; 166 AA

Human soluble CD23 isoform 17-JUN-1997 (first entry)

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                                               (LYNC/) LYNCH R G.
(MATS/) MATSUI M.
(NUNE/) NUNEZ R M.
(YODO/) YODOI J.
DNA sequence encoding a soluble isoform of CD23 - useful for large scale preparation of the protein
                        WPI; 1997-159094/15.
N-PSDB; AAT61959.
                                                                                       28-DEC-1994;
                                                                                                     27-DEC-1995;
                                                                                                                     04-FEB-1997.
                                                                                                                                     JP09028385-A
                                                                                                                                                    Homo sapiens
                                                                                                                                                                    isoform D; recombinant production.
                                                                                                                                                                            Human; soluble; CD23; complementarity determining;
                                                                                      94US-0365103
                                                                                                     95JP-0341169
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RESULT 2
AAW13148
ID AAW1
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(MATS/) MATSUI M.
(NUNE/) NUNEZ R M.
(YODO/) YODOI J.
                                                                                                                                                                                           The specification states that the nucleotide sequences contained in figures 4a-b, 5a-b, 12a-12b and 13a-b are claimed, however this numbering scheme does not relate to the scheme used in the relevant sections of the specification.
                                                                                                                                                                                                                                                                                            The cDNA encoding the present sequence, human soluble CD23 isoform C, can be used for the large scale recombinant pro of soluble CD23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The specification states that the nucleotide sequences contained in figures 4a-b, 5a-b, 12a-12b and 13a-b are claimed, however this numbering scheme does not relate to the scheme used in the relevant sections of the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The cDNA encoding the present sequence, human soluble CD23 isoform D, can be used for the large scale recombinant proof soluble CD23.
                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Figure 15; 33pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA sequence encoding a soluble isoform scale preparation of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-159094/15.
N-PSDB; AAT61961.
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isoform C; recombinant production.
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                                                  l Similarity
12; Conserv
                                                                                                                                                167 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
Peptide
                                                                                                                                                                                                              The CDNA encoding the present sequence, which contains human soluble CD23 isoform B, can be used for the large scale recombinant production of soluble CD23.

The specification states that the nucleotide sequences contained in figures 4a-b, 5a-b, 12a-12b and 13a-b are claimed, however this numbering scheme does not relate to the scheme used in the relevant sections of the specification.
                                                AAP70105;
                                                                  AAP70105 standard;
                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                            Claim 1; Pages 18-20; 33pp; Japanese.
                                                                                                                                                                                                                                                                                                                DNA sequence encoding a soluble isoform scale preparation of the protein
                                                                                                                                                                                                                                                                                                                                            WPI; 1997-159094/15.
N-PSDB; AAT61956.
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isoform B; recombinant production.
          IgE binding factor
                             04-FEB-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence containing human soluble CD23 isoform B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-JUN-1997
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                                                                                                                   95
                                                                                                                                                                Local
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                                                                                                                                     2 RAEQORLKSQDL 13
                                                                                                                  RAEQQRLKSQDL 106
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                            (first entry)
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                                                                  protein;
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100.0%; Pr
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                                                                                                                                                                Score 57;
Pred. No.
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                                                                                                                                                        Mismatches
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RESULT 5
AAP82073
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Best Local Similarity
Thehes 12; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-APR-1986;
04-SEP-1986;
05-SEP-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The protein reacts with anti-Fc epsilon receptor antibody, and is obtd. in large quantities. The DNA encoding the protein is obtd. from, eg human B cells, human malignant B or T cells, human monocytes or human eosinophilic cells. RRMI 8866 cells may also be cultured to produce the mRNA. The IgE binding factor and Fc epsilon receptor binds IgE and can be used to enhance the produc. If IgE from IgE producing cells. They can be used to treat allergies by eliminating excess blood IgE, and can also
   Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                     AAP82073;
                                                                                                                                                                                                                                                                                                                                                                                                                    AAP82073 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 6; page 42-3; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAN70107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Honjo T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-APR-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-DEC-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                   Modified-site
                                                                                                     Domain
                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                   Low affinity Fc
                                                                                                                                                                                                                                                                                                                    Recombinant
                                                                                                                                                                                                                                                                                                                                                   17-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (KURS ) KURARAY CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IgE binding
                                                                                                                                                                                                    Domain
                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96 RAEQQRLKSQDL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 RAEQORLKSQDL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IgE binding factor protein - obtd. by culturing cells harbouring a ss specific Fc receptor on their surface.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1987-343202/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yodoi J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        321 AA;
                                                                                                                                                                                                                                                                                                                  Fc_epsilon receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              factor;
                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86JP-0101531.
86JP-0209091.
86JP-0210429.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87EP-0106265
                                                 /label-transmembrane region /note-"hydrophobic residues" 63..63
                                                                                                                                                                                                                                                                                 epsilon
 /label*glycosylation_site
/note="N-linked"
149..150
                                                                                                               /label-stop_transfer_seq
/note-"basic cluster involved
integration into bilayer"
                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                 /note="hydrophilic N-terminal"
                                                                                                                                                                                                                                                                                                                                                                                                                   protein; 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Takami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          epsilon receptor; allergy; RPMI 8866 cells;
                                                                                                                                                                                                                                                                                   receptor; IgE; allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Z
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 57;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                    ⋛
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 8;
0.1;
                                                                                                                                  in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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RESULT 6
AAP81163
ID AAP8
XX
AC AAP
DT 15-(
DT LOW
XX
XX
HOT
OX
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Best Local
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P-PSDB; AAP82073.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kishimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-SEP-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-MAR-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP258489-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
                                WPI; 1988-057531/09
N-PSDB; AAN81485.
                                                                                                                                                                                                                                                                                                                Low affinity
                                                                                                                                                                                                                                                                                                                                                 Low affinity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
 New human lower affinity Fc(epsilon)-receptor - useful for treating
                                                                                  Kishimoto T,
                                                                                                                 (KISH/) KISHIMOTO T.
                                                                                                                                                21-AUG-1986;
                                                                                                                                                                                 21-AUG-1986;
                                                                                                                                                                                                                  02-MAR-1988
                                                                                                                                                                                                                                                  EP257114-A.
                                                                                                                                                                                                                                                                                   Homo
                                                                                                                                                                                                                                                                                                                                                                                    15-0CT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                    AAP81163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAP81163 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CELL-) CELLULAR IMMUNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-AUG-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96 RAEQQRLKSQDL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 RAEQORLKSQDL 13
                                                                                                                                                                                                                                                                                 sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ŧ,
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                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                  Suemura
                                                                                                                                                86EP-0111581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86EP-0111581
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DNA encoding the sequence or a part of it can be used to make recombinant receptor which is useful for treating IgE allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Page 39; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human low affinity Fc(epsilon)-receptor and parts for treating local or systemic allergic reactions and recombinant DNA methods.
                                                                                                                                                                                                                                Fc_epsilon receptor; IgE; allergy.
                                                                                                                                                                                                                                                                 Fc_epsilon receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label=soluble
/note="Claim 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label=membrane_bound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="target for trypsin-like proteases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.9%; st.
100.0%; Pr
Kikutani H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kikutani H,
                                                                                                                                                                                                                                                                                                                                                                      321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 57;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                    Å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                 encoded by gene carried by pGEM4.
Barsumian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 9;
0.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - useful
obtd. by
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ARESULT 7
AAAB1230
ID AAAB8
XX AAAB8
XX AAAB8
XX 25-0
DX FC 9
XX FC 9
XX JP63
PN JP63
PN JP63
PN JP63
PR 05-S
PR 05-S
PR 05-S
PR 04-A
XX 24-A
XX 24-A
XX 19E
DR N-PS
XX 19E
DR N-PS
XX 19E
CC 1E 19E
CC 1E 16
CC of t
XX Sequ
RESULT 8
AAP81112
ID AAP8
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AC AAP8
AC AAP8
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DT 12-D
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Huma
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                                                                                                                                                                                                                                                   Query Match 91.9
Best Local Similarity 100
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                Fc epsilon receptor binds IgE. It is e
It is expressed in large amts and can
blood, and to detect and quantify IgE.
of therapy and diagnosis of allergy.
Human IgE binding factor related polypeptide.
                                  12-DEC-1990
                                                                   AAP81112;
                                                                                                  AAP81112 standard;
                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; ge 529; 16pp; japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New DNA contg. nucleotide sequence encoding Fc epsilon receptor for obtaining IgE-binding substance used to detect and quantify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1988-273895/39
N-PSDB; AAN81612.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-SEP-1986;
24-APR-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-APR-1987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fc epsilon receptor; IgE; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fc gamma receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        local and allergic reactions produced by the expression of IgE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (KURS ) KURARAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAP81230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAP81230 standard;
                                                                                                                                                                                     96 RAEQORLKSQDL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96
                                                                                                                                                                                                                      2 RAEQQRLKSQDL 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      responsible for allergies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RAEQQRLKSQDL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 24;
                                                                                                                                                                                                                                                                                                                     321 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          321 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first
                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86JP-0210429
87US-0042445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36pp; English
                                                                                                  peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein;
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                                                                                                                                                                                                                                                                   91.98;
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                                                                                                                                                                                                                                                     Score 57; DB; Pred. No. 0.1
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                   expressed from cell line RPMI8866.

n be used to remove excess IgE from

This would allow the development
                                                                                                                                                                                                                                                                    DB 9;
0.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 9;
0.1;
                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                  Length 321;
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                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                     0;
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AAP81172
   PRESENTACION DE CONTRACTOR DE 
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
11-APR-1987;
21-AUG-1986;
                                                06-AUG-1987;
                                                                                 16-MAR-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                 EP259615-A.
                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                     28-MAR-1992
                                                                                                                                                                                                                                                                                                                                      AAP81172;
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07-NOV-1986;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                 therapy.
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The peptide is related to the IgE receptors on human B-cells and, if without the membrane anchoring sequence, to the IgE-BFs of Sarfati et al. Immunology 53, 197, 207, 783 (1984).

Amino acids between 1-133 starting from the N-terminal may be deleted. This is the membrane-anchoring sequence binding the polypeptide to the cytoplasmic membrane of the B-cells.

Alternatively amino acids between 110-130 or 250-321 may also be deleted. Alternatively amino acids between 110-130 or sequence such as pollens, e.g. as caused by antigens such as pollens,
                                            Sequence encoded by a gene for the water-soluble part of the human low affinity Fc-epsilon-receptor with the amino acids 150 to 321, comprising the EcoRI insert from pFc-epsilon-R-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 36; 48pp;
                                                                                                                                                                                                                                 AAP81172 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cat danders and house dust mites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New IgE binding factor related polypeptide(s) - produced by recombinant methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAN81437.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1988-022917/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hofstetter H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human IgE binding factor; IgE-BFS; allergic diseases; B-cells
ow affinity Fc-epsilon-receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CIBA ) CIBA
                                                                                                                                                                                                                                                                                                                                             l Similarity
12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              321 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GEIGY AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kilchherr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86GB-0017862
86GB-0026622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87EP-0110458
                                                                                                                                                                                                                                    Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            91.9%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H
                                                                                                                                                                                                                                    321
                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 57;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
    systemic IgE-allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 9;
0.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 321
                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
       reaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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87EP-0105425 86EP-0111581 87EP-0111392

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RESULT 10
AAP90120
XX AAP90
XX AAP90
XX O1-NO
XX Human
XX Human
XX Human
XX Homo
XX Ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The inventors claim a human low affinity Fc-epsilon-receptor (FCR)

Wilh an N-terminal cytoplasmic domain, a C-terminal extracellular

Commain and a mol.wt. of about 46kd. Also claimed are recombinant DNA

Conty. the genetic information for the FCR, vectors conty. the DNA,

Conty. the genetic information for the FCR, vectors conty. The DNA,

Const organisms transformed with the vectors, oligonucleotides coding

for partial amino acid sequences from FCR, and processes for

preparing FCR. Preferred embodiments of the present invention are

preparing FCR. Preferred embodiments of the present invention are

preparing FCR. Preferred embodiments of the FC-epsilon-R

C part of the cDNA SQ coding for the AMS 1 to 148 of the FC-epsilon-R

C part of the cDNA SQ coding for the AMS 1 to 148 of the FC-epsilon-R

C signal SQ e.g.by the BSF-2 signal SQ (see pBSF-2-L8-AAN81517/P81176).

A suitable yeast expression vector is a plasmid conty. the yeast

ADHI-promoter, a gene coding for the yeast matting factor alpha

leader peptide (MF alpha leader SQ) a multicloning site and the

yeast ADHI-terminator (see AAN81514/P81173). See also EP-258492.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-SEP-1986;
05-DEC-1986;
06-AUG-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human lymphocyte receptor
asthma; immunoglobulin E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant human low affinity Fc(epsilon)- receptor - used for the treatment of local and systemic IGE-allergic reactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kishimoto T,
  WPI; 1989-214148/30.
                                                     Kishimoto T,
Schwendenwein
                                                                                                                                                                                          20-JAN-1988;
                                                                                                                                                                                                                                             20-JAN-1988;
                                                                                                                                                                                                                                                                                                  26-JUL-1989
                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human lymphocyte receptor for immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAP90120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAP90120 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAN81512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (KISH/) KISHIMOTO T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 RAEQQRLKSQDL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RAEQQRLKSQDL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1988-072124/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l Similarity
12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OSAKA UNIVERSITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Table 3, Page 79-81; 118pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   321 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry
                                                                                                                                                                                                                                                                                                                                                                                                             (Human)
                                                  Suemura M, Kikutani H, Bar
R, Sommergruber W, Swetly
                                                                                                                                    UNIVERSITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Suemura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86EP-0113073.
86EP-0116938.
87EP-0111392.
                                                                                                                                                                                          88EP-0100814
                                                                                                                                                                                                                                             88EP-0100814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kikutani H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for immunoglobulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 57;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
                                                  Barsumian
tly P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barsumian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 9;
0.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypersensitivity; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 321;
                                                                               EL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                               Schneider F-J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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RESULT 12 AAR42053 ID AAR42

AAR42053 standard; Protein; 321 AA

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RESULT 11
AAP90367
ID AAP90367
AC AAP90
XX AP90
XX 01-NC
XX Pept1
XX Fc ep
XX Fc ep
XX EP321
XX EP321
XX EP321
XX EP321
XX CSAU
XX CSAU
XX CSAU
XX C1one
PT C0din
PX C1one
PT C1one
XX The k
XX The k
XX Squeen
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                                      Matches
                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Soluble recombinant Fc-epsilon receptor - used for treatment or prophylaxis of local and allergic reactions induced by IgE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Whole human lymphocyte receptor for immunoglobulin (see corres AAN90344). Used to produce highly bloactive water-soluble FCR. Water-soluble FCR binds IgE, so it useful for treating hypersensitivity, esp. asthma. Amino acid residue 150 is a possible site for trypsin-like proteases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAN90344.
                                                                                                                                    Cloned genes coding for soluble IgE receptor - coding sequence of Fc epsilon receptor gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; fig 1; 23pp; English.
                                                                            Sequence
                                                                                              The known
                                                                                                                   Disclosure;
                                                                                                                                                                  N-PSDB;
                                                                                                                                                                           WPI; 1989-186101/26.
                                                                                                                                                                                               Kishimoto
                                                                                                                                                                                                                (OSAU ) OSAKA UNIVERSITY
                                                                                                                                                                                                                                      22-DEC-1987;
                                                                                                                                                                                                                                                       22-DEC-1987;
                                                                                                                                                                                                                                                                           28-JUN-1989
                                                                                                                                                                                                                                                                                               EP321601-A.
                                                                                                                                                                                                                                                                                                                  Fc epsilon
                                                                                                                                                                                                                                                                                                                                   Peptide sequence of
                                                                                                                                                                                                                                                                                                                                                        01-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                           AAP90367;
                                                                                                                                                                                                                                                                                                                                                                                             AAP90367 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                              96
96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                Local
                  N
                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 RAEQQRLKSQDL
                  RAEQQRLKSQDL
                                                                                                                                                                                                                                                                                                                                                                                                                                              RAEQQRLKSQDL
RAEQQRLKSQDL
                                      l Similarity
12; Conserv
                                                                                                                                                                 AAN90134, AAN90135, AAN90136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                               Ή
                                                                                              peptide sequence of Fc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           321
                                                                            321
                                                                                                                                                                                                                                                                                                                receptor; cloned gene; IgE; allergy; ,asthma
                                                                                                                 fig 1; 19pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                      Conservative
                                                                                                                                                                                                                                                                                                                                                       (first
                                                                                                                                                                                              Suemura M,
                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A
A
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                                                                                                                                                                                                                                                        87EP-0119080
107
                  13
                                                                                                                                                                                                                                                                                                                                                                                                                                              107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13
                                                                                                                                                                                                                                                                                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                    mutated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91.9%;
                                               91.9%;
                                                                                                                  English.
                                                                                                                                                                                               Kikutani H,
                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                   Fc epsilon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 57;
Pred. No.
                                               Score Pred.
                                                                                                                                                                                                                                                                                                                                                                                              321
                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                               ξ
                                                                                              epsilon receptor
                                                        57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No.
                                                 Z
O
                                                                                                                                                                                               Barsumian
                                                                                                                                                                                                                                                                                                                                    receptor
                                                0 B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DВ
                                          0.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                              comprising modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 321;
                                                        Length
                                                                                                                                                                                               M
                                                                                              gene
                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                      0
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RESULT 13
AAW13142
ID AAW13
XX
AC AAW13
XX
DT 17-JU
XX
DE Seque
XX
Human
KW Human
KW Homo
XX
Homo
XX
FT Pept!
YT
PN JF091
XX
PF 37-D
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                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 12
                     04-FEB-1997
                                                                                                                                             Sequence containing human soluble CD23 isoform
                                                                                                                                                                  17-JUN-1997
                                                                                                                                                                                    AAW13142;
                                                                                                                                                                                                      AAW13142 standard;
                                                                                                                                                                                                                                                                                                                                                  The sequence is of IgE-binding factor, secreted from the plasmid pSVG-BF. The plasmid pSVG-BF is a derivative of plasmid pSVG-ER which has the sequence coding amino acids 1-147 replaced with a coding region (AAQS5400) allowing secretion of the factor.
                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant DNA molecule - comprises enhancer and promoter unit
linked to transcriptive DNA segment and DNA segment comprising
promoter unit linked to DNA sub-segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IgE;
 27-DEC-1995;
                                       JP09028385-A
                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1993-275121/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-DEC-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-DEC-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-JUL-1993
                                                                   Peptide
                                                                                                                            Human; soluble;
                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 28; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IL84702-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IgE binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR42053;
                                                                                                                  isoform A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CIBA ) CIBA GEIGY AG
                                                                                                                                                                                                                                                     96
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                                                                                                                                                                                                                                                               RAEQQRLKSQDL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    binding
                                                                                              sapiens
                                                                                                                                                                                                                                                     RAEQORLKSODL 107
                                                                                                                                                                                                                                                                                         ch 91.9%;
l Similarity 100.0%
12; Conservative
                                                                                                                 recombinant
                                                                                                                                                                                                                                                                                                                                 321 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       factor
                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    factor; secretion; expression; signal sequence
 95JP-0341169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87IL-0084702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   871L-0084702
                                                                                                                            CD23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
148..321
/label= IgE-binding
                                                                   Location/Qualifiers
1..205
                                                                                                                                                                                                      Protein;
                                                                                                                 complementarity t production.
                                                         "soluble CD23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IgE-binding_factor
                                                                                                                                                                                                                                                                                                   .08;
                                                                                                                                                                                                      321
                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                   Score 57;
Pred. No.
                                                                                                                                                                                                      β
                                                                                                                                                                                                                                                                                          Mismatches
                                                          isoform
                                                                                                                           determining,
                                                                                                                                                                                                                                                                                                  DB 14;
0.1;
                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                             Length 321;
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                                                                                                                                                                                                                                                                                         Gaps
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AAP82839
ID AAP82839
ID AAP82839
ID AAP82839
AC AAP82
AC 
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(MATS/) MATSUI M.
(NUNE/) NUNEZ R M.
(YODO/) YODOI J.
                        This protein is useful in the treatment of local or systemic IgE-allergic reactions and is obtd. by recombinant DNA methods. It is pref. un-accompanied by associated native glycosylation. Fragments it can also be used. See also AAN82253.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       production of soluble CD23

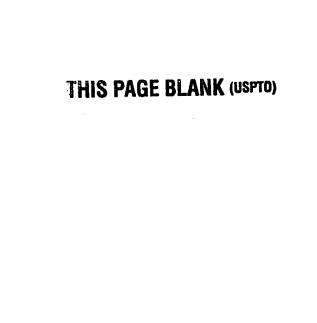
The specification states that the nucleotide sequences contained in figures 4a-b, 5a-b, 12a-12b and 13a-b are claimed, however this in figures 4a-b, one claimed to the scheme used in the relevant
                                                                                                                                        Disclosure; ; pp;
                                                                                                                                                                                      New human low affinity Fc(epsilon)-receptor and parts treating local or systemic IgE-allergic reactions and recombinant DNA methods.
                                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                         Kishimoto T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-DEC-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-DEC-1986;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fc(epsilon) receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human low affinity Fc(epsilon) receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The cDNA encoding the present sequence, soluble CD23 isoform A, can be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Pages 16-17; 33pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA sequence encoding a soluble isoform scale preparation of the protein
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N-PSDB; AAT61955.
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DB; AAN82252.
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                                                                                                                                        English.
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Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The cDNA is obtained by reverse transcription of mRNA isolated from cells expressing IgB-binding activity, esp. human B-cells RPMI 8866. The peptide is related to the IgB receptors on human B-cells and, if without the membrane anchoring sequence, to the IgE-BFs of Sarfati et al. Immunology 53, 197, 207, 783 (1984).

Amino acids between 1-133 starting from the N-terminal may be deleted. This is the membrane-anchoring sequence binding the polypeptide to the Cytoplasmic membrane of the B-cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                      Alternatively amino acids between 110-130 or 250-321 may also be deleted. The peptide has IgE binding activity and is useful tor treating deleted conditions, e.g. as caused by antigens such as pollens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-JUL-1986;
07-NOV-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human IgE binding factor; IgE-BFs; allergic diseases; pCL-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human IgE binding factor related polypeptide from pCL-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence has the formula of AAP\theta1112 wherein the amino acids 106\mbox{-}127 are deleted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; ; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         recombinant methods.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAN81438.
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                                                                                                                                                                                                 Local Similarity 91.7 nes 11; Conservative
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ALIGNMENTS

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nimum DB seq ximum DB seq	length: 0 length: 2000000000		IGE FC receptor II, low-affinity (validated) - hum	10
st-processing:	g: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	ies	N;Alternate names: bidSt-2; CD3; *C'epSilon**x1; lymphotyte ign receptor N;Contains: IgE Fc receptor II, splice form a; IgE Fc receptor II, splice C;Species: Homo sapiens (man) C:Date: 31-Mar-1988 *sequence revision 31-Mar-1988 *text change 15-Sep-20	For receptor II, splice form a'; Ig #text change 15-Sep-2000
tabase :	IR_73:	<i>t</i> .	u co	067; S03279; S39442; S39443; A26164; A26589; A31924; JL0132; S29107 Inui, S.; Sato, R.; Barsumian, E.L.; Owaki, H.; Yamasaki, K.; Kaisho,
	2: pir2: * 3: pir3: * 4: pir4: *		A;Title: Molecular structure of human lymphocyte receptor for immunoglobulin E. A;Reference number: A26067; MUID:87051737; PMID:2877743 A;Accession: A26067	sceptor for immunoglobulin E. 77743
Pred. No score gr and is c	. is the number of results eater than or equal to the erived by analysis of the	No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution.	A; Residues: 1-321 <kik> A; Cross-references: GB:M14766; NID:g182449; PIDN:AAA52435.1; PID:g18245 A; Experimental source: EBV-transformed B lymphoblastoid cells RPMI-8866</kik>	AA52435.1; PID:g182450 stoid cells RPMI-8866
		SUMMARIES	Nucleic Acids Res. 15, 725-7308, 1987	too too of the burns
sult No. Score	Query Match Length DB ID	Description	A; Accession: S03279	- тапктиў теўтой от сле лиман тумр
1 57	9 321 1	י פר	A;Status: nucleic acid sequence not shown; not compared with A;Molecule type: DA: A: Doc:41.00: 157-204 / Crimo	pared with conceptual translation
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5 5 4 4 1 1	66.1 234 2 B44459	T, cardi	n sequer	complete sequence is not shown odoi, J.
	1 249 2		A; Title: Alternative transcripts of the human CD23/Fc-epsilon-RII.	/Fc-epsilon-RII. A possible novel m
9 41	1 251 2	H H	A; Reservence number: \$39442; MOID:94063078; PMID:83 A; Accession: \$39442	3004
11 41	1 253 2	troponin T, tast s troponin T, skelet	A; Molecule type: DNA A; Residues: 1-7, 'D', 47-50 <mas1></mas1>	
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16 41 17 41	1 274 2 1 284 2	T, skele T, cardi	<pre>A;Experimental source: splice form b' R;Ludin, C.; Hofstetter, H.; Sarfati, M.; Levy, C.A.; Suter,</pre>	.; Suter, U.; Alaimo, D.; Kilchher
	66.1 289 2	, H	EMBO J. 6, 109-114, 1987	1
20 41	66.1 298 1	, e	A; Title: Cioning and expression of the clun coding for a numan lymphocyte A; Reference number: A26164; MUID:87218454; PMID:3034567	ror a numan lymphocyte ig£ recepto 34567
	64.5 248	tropomyosin 4, fib	A; MCCESSION: AZOTO4 A; MCCESSION: AZOTO4	
	62.9 278 1 62.9 309 1	troponin T, slow s IgE Fc receptor II	A; Residues: 1-268, 'T', 270-321 <lud> A; Cross-references: GB: X04772; NID: g34002; PIDN: CI</lud>	\28465.1; PID:g34003
	62.9 1691 1 61.3 146 2	genome polyprotein	A; Note: the codon given for 269-Asn (ACC) is incor	sistent with the authors' translati
	61.3 157 2		R; Ikuta, K.; Takami, M.; Kim, C.W.; Honjo, T.; Miyoshi, T.; Tagaya, Y.; Kawabe, T.; Y	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
	OL.3 230	hypothetical prote		oshi, T.; Tagaya, Y.; Kawabe, T.; Y

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A;Cross-reterences: oursilious, A;Cross-reterences: oursilious, A;Map position: 19p13.3-19p13.3

A;Map position: 19p13.3-19p13.3-19p13.3

A;Introns: 8/1; 46/1; 64/1; 85/1; 105/1; 127/1; 157/1; 207/3; 243/2

C;Superfamily: IgE receptor II; C-type lectin homology

C;Superfamily: IgE receptor II; C-type lectin; immunoglobulin receptor; macroph

F; MNPPSQD; 47-221/Product: IgE FC receptor II, splice form b' #status predicted <SFB>
F; MNPPSQD; 47-221/Product: IgE FC receptor II, splice form b #status predicted <SFB>
F;1-321/Product: IgE FC receptor II, splice form a *status predicted <SFB>
F;1-7, 'D', 47-321/Product: IgE FC receptor II, splice form a *status predicted <SFB>
F;1-7, 'D', 47-321/Product: IgE FC receptor II, splice form a *status predicted <SFB>
F;1-7, 'D', 47-321/Product: IgE FC receptor II, splice form a *status predicted <SFB>
F;1-7, 'D', 47-321/Product: IgE FC receptor II, splice form a *status predicted <SFB>
F;1-7, 'D', 47-321/Product: IgE FC receptor II, splice form a *status predicted <SFB>
F;1-7, 'D', 47-321/Product: IgE-binding factor (37K) #status predicted <SFBI>
F;64-84/Region: 21-residue repeat
F;102-221/Product: soluble IgE-binding factor (37K) #status predicted <IGE>
F;150-321/Product: soluble IgE-binding factor (25-27K), long form #status experimental
F;149-150/Cleavage site: Lys-Leu (unidentified proteinase) #status experimental
F;149-150/Cleavage site: Arg-Met (unidentified proteinase) #status experimental
F;149-150/Cleavage site: Arg-Met (unidentified proteinase) #status experimental
F;147-148/Cleavage site: Arg-Met (unidentified proteinase) #status experimental
F;149-150/Cleavage site: Arg-Met (unidentified proteinase) #status experimental
F;149-150/Cleavage site: Arg-Met (unidentified proteinase) #status experimental
F;149-150/Cleavage site: Arg-Met (unidentified proteinase) #status experimental
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A;Title: Partial characterization of natural and recombinant human soluble CD23. A;Reference number: S29107; MUID:93038513; PMID:1417742
A;Accession: S29107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the Brookhaven Protein Data Bank, November 1995
A;Reference number: A65963; PDB:IKUE
A;Contents: annotation; conformation by theoretical model, residues 173-285
C;Comment: The sequence of the splice form a is shown.
C;Comment: This receptor for the Fc portion of IgE is expressed in various hematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 'MNPPSQ',8-14 <YOK>
A;Cross-references: GB:M23562; NID:9182444
A;Cross-references: GB:M23562; NID:9182444
A;Experimental source: splice form IIb
R;Letellier, M.; Sarfati, M.; Delespesse, G.
Mol. Immunol. 26, 1105-1112, 1989
A;Title: Mechanisms of formation of IgE-binding factors (soluble CD23)-I. Fc epsilon A;Reference number: JL0132; MUID:90220658; PMID:2534424
A;Accession: JL0132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: GDB:FCER2; FCE2
A;Cross-references: GDB:118888; OMIM:151445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Comment: Splice form a is expressed constitutively in B-cells; b is expressed in C;Comment: Soluble IgE-binding factors are produced by proteolytic cleavage of IgE
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A;Accession: A31924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A26589; A; Accession: A26589
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A; Residues: 152-166; 173-179; 189-212; 230-263; 268-306
R; Padlan, E.A.; Helm, B.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein A; Residues: 1-321 <LET>
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                                                Best
Matches
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Match

91.98;

Score 57;

DB 1;

Length 321;

Local

Similarity
9; Conser

Conservative

Indels

0;

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0

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A; Molecule type: DNA
A; Residues: 1-756 < WHI>
A; Cross-references: GB: AE001863;
A; Cross-references: GB: AE01863;
                                                                         A;Gene:
A;Map pc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 68-302 <CO2>
A;Cross-references: GB:K02263; NID:g212781; PIDN:AAA49098.1; PID:g212782
C;Comment: This protein, found in adult cardiac muscle and transiently in and skeletal muscle. Down-regulation of the protein in the late stages of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Cooper, T.A.; Ordahl, C.P.
J. Biol. Chem. 260, 11140-11148, 1985
A;Title: A single cardiac troponin T gene generates embryonic
A;Reference number: A25373; MUID:85289327; PMID:2993302
A;Accession: A25373
                                                                                                                                                                                                                                          M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; S.; Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium A;Reference number: A75250; MUID:20036896; PMID:10567266 A;Accession: F75590
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: troponin T
C;Keywords: alternative splicing; cardiac muscle; differentiation; heart; muscle; pho F;1-302/Product: troponin T, cardiac muscle, embryonic splice form #status predicted F;1-22,33-302/Product: troponin T, cardiac muscle, adult splice form #status predicte
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                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                   R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K., M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                          methyl-accepting chemotaxis-related protein - Deinococcus radiodurans (strain C;Species: Deinococcus radiodurans C;Date: 03-Dec:1999 #sequence_revision 03-Dec:1999 #text_change 31-Mar-2000 C;Accession: E75590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: A single troponin T gene regulated by different programs in cardiac A;Reference number: A03086; MUID:85065747; PMID:6095446 A;Accession: A03086
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Science 226, 979-982,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:M10013; NID:g212783; PIDN:AAA49099.1; R:Cooper, T.A.; Ordahl, C.P.
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A; Residues: 1-302 <COO>
                         Query Match
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mes 8; Conserv
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72.7%;
  69.4%;
69.2%;
                                                                                                                                                                        GB:AE001825; NID:g6460670; PIDN:AAF12432.1;
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Score 43;
Pred. No.
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Pred. No.
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                         Length 756;
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skeletal m
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troponin T, fast skeletal muscle splice form alpha - rabbit (fragment) C:Species: Oryctolagus cuniculus (domestic rabbit) C:Date: 30-Apr-1993 #sequence_revision 17-May-1996 #text_change 17-May-199 C:Accession: B44459
R;Pan, B.S.; Potter, J.D.
J. Biol. Chem. 267, 23052-23056, 1992
A:Title: Two genetically expressed troponin T fragments representing alpha A;Reference number: A44459; MUID:93054628; PMID:1429653
A;Recession: B44459
A;Status: nucleic acid sequence not shown; not compared with conceptual tr A;Molecule type: mRNA
A;Residues: 1-234 <PAN>
A;Residues: 1-234 <PAN>
A;Residues: 1-234 <PAN>
A;Residues: Sequence extracted from NCBI backbone (NCBIP:118207)
C;Comment: The two carboxyl-terminal isoforms of troponin T are designated expression of troponin T.
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A; Cross references: EMBL:
C; Genetics:
A; Introns: 14/2
C; Superfamily: troponin T
C; Keywords: cardiac muscl
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A; Molecule type: mR
RESULT 6
A34327
A34327
C:Species: Coturnix coturnix japonica (Japanese quail)
C:Species: Coturnix coturnix japonica (Japanese quail)
C:Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change
C:Accession: A34327
C:Baucher, E.A.; Charles de la Brousse, F.; Emerson Jr., C.P.
F:Bucher, E.A.; 12482-12491, 1989
A;Title: Developmental and muscle-specific regulation of avian fa;Reference number: A34327; MUID:89308680; PMID:2745456
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C;Keywords: alternative splicing;
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troponin T, fast skeletal muscle splice form beta .C;Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 C;Accession: A44459; 145517 R;Pan, B.S.; Potter, J.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: A34327
A;Status: preliminary
A;Nolecule type: mRNA
A;Residues: 1-249 <BUC>
A;Cross references: GB:M26599; NID:g213627;
C;Superfamily: troponin T
C;Keywords: skeletal muscle
                                                                                                                                                                                                        troponin T, cardiac muscle (clone TNT6-1) - human C;Species: Homo sapiens (man) C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995
                                                                                                                                                                                                                                                                   RESULT
S48793
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A; Residues: 1-249 < PAN>
A; Residues: 1-249 < PAN>
A; Residues: 1-2549 < PAN>
A; Residues: 1-2549 < PAN>
A; Residues: neonatal skeletal muscle
A; Note: sequence extracted from NCBI backbone (N
R; Putney, S.D.; Herlihy, W.C.; Schimmel, P.
Nature 302, 718-721, 1983
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A;Accession: A44459
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A44459
A; Residues: 1-250 <FAR>
A; Cross references: EMBL:X79861; NID:g587427;
C; Superfamily: troponin T
C; Keywords: cardiac muscle; heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Superfamily: troponin T C; Keywords: alternative splicing; differentiation; skeletal muscle
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                                                                                                           A; Reference number: A; Accession: $48793
                                                                                                                                submitted to the EMBL Data A; Reference number: S48790
                                                                                                                                                                      C; Accession: S48793
R; Farza, H.
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A; Residues: 207-226 < PUT>
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                                                                           A; Molecule type: mRNA
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ERAEQORIRAE 103
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troponin T, skeletal muscle, isoform 4 - chicken
C:Species: Gallus gallus (chicken)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change
C:Accession: D31957
C:Rimillie, L.B.; Golosinska, K.; Reinach, F.C.
J. Biol. Chem. 263, 18816-18820, 1988
A;Title: Sequences of complete cDNAs encoding four variants of cA;Reference number: A92698; MUID:89066672; PMID:3198600
A;Recession: D31957
A;Molecule type: mRNA
A;Residues: 1-251 CSMI>
A;Residues: 1-251 CSMI>
A;Residues: 1-251 CSMI>
troponin T, skeletal muscle, isoform 2 - chicken C;Species: Gallus gallus (chicken) C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_cha C;Accession: B31957 R;Smillie, L.B.; Golosinska, K.; Reinach, F.C. J. Biol. Chem. 263, 18816-18820, 1988 A;Title: Sequences of complete cDNAs encoding four variants A;Reference number: A92698; MUID:89066672; PMID:3198600 A;Accession: B31957
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R;Bucher, E.A.; Charles de la Brousse, F.; Emerson Jr., C.P.
J. Biol. Chem. 264, 12482-12491, 1989
A;Title: Developmental and muscle-specific regulation of avian fast skeleta A;Reference number: A34327; MUID:89308680; PMID:2745456
A;Accession: B34327
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B31957
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A; Residues: 1-253 <BUC>
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7; Conserv
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RESULT
TPRBTS
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A;Molecule type: mRNA
A;Residues: 1-257 <SMI>
A;Residues: 1-257 <SMI>
A;Cross-references: GB.M22155; GB:J04198; NID:g212787; PIDN:AAA49101.1; PID:g212788
C;Superfamily: troponin T
C;Keywords: alternative splicing; muscle; phosphoprotein; skeletal muscle
                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-263 <SMI>
A;Cross-references: GB:M22156; GB:J04198; NID:g212789; PIDN:AAA49102.1; PID:g212790
C;Superfamily: troponin T
C;Keywords: alternative splicing; muscle; phosphoprotein; skeletal muscle
                                                                                                                                                                                                                                                                                              troponin T, skeletal muscle, isoform 3 - chicken c;Species: Gallus gallus (chicken) C;Date: 31-Mar-1990 *sequence_revision 31-Mar-19 C;Accession: C31957 R;Smillie, L.B.; Golosinska, K.; Reinach, F.C.
                                                                                                                                                                                                                          J. Biol. Chem. 263, 18816-18820, 1988
A;Title: Sequences of complete cDNAs encoding four variants
A;Reference number: A92698; MUID:89066672; PMID:3198600
A;Accession: C31957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               troponin T - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 *sequence,
C;Accession: I53021
R;Wu, Q.L.; Jha, P.K.; Raychov
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A;Map position: 11p15.5-11p15.5
C;Superfamily: troponin T
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                                                                   Conservative
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troponin
N;Contain
C;Species
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A.Residues: 1-21.39-53 <BR3>
R:Moir, A.J.G.; Cole, H.A.; Perry, S.V.
Biochem. J. 161, 371-382, 1977
A:Title: The phosphorylation sites of troponin T from white skeletal muscle and the effet A:Reference number: A90295; MUID:77157104; PMID:849266
A:Reference number: phosphorylation sites A:Note: phosphorylation under in vivo conditions occurred at positions that may not be a R:Putney, S.D.; Herlihy, W.C.; Schimmel, P.
Rature 302, 718-721, 1983
A:Title: A new troponin T and cDNA clones for 13 different muscle proteins, found by she A:Reference number: 146471; MUID:83167564; PMID:6687628
A:Reference number: 146471; MUID:83167564; PMID:6687628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Description: binds the troponin complex to tropomyosin; with tropomyosin mediates A;Pathway: muscle contraction C;Superfamily: troponin T C;Keywords: acetylated amino end; alternative splicing; differentiation; muscle cont C;Keywords: acetylated amino end; alternative splicing; differentiation; muscle cont C;Keywords: acetylated amino end; alternative splice form 1 *status experimenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Briggs, M.M.; Schachat, F. 7. Mol. Biol. 206, 245-249, 1989
A;Title: N-terminal amino acid sequences of three functionally different troponin A;Reference number: S03590; MUID:89199646; PMID:2704041
A;Accession: S03590
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C;Date: 24-Apr-1984 #sequence_revision 17-May-1996 #text_change 22-Jun-1999
C;Accession: A03083; S03590; S03591; S03592; I46515; I46516
R;Pearlstone, J.R.; Johnson, P.; Carpenter, M.R.; Smillie, L.B.
J. Biol. Chem. 252, 983-989, 1977
A;Title: Primary structure of rabbit skeletal muscle troponin-T. Sequence determination A;Reference number: A92220; MUID:77118575; PMID:320204
A;Accession: A03083
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A;Cross-references: EMBL:V00900; NID:g1742; PIDN:CAA24265.1;
C;Complex: troponin is a heterotrimer with one molecule each C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
A; Residues: 1-10,17-18,'E',20-48,50-266 <PE2>
A; Note: this is the final paper in a series
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A;Accession: 146516
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A; Residues: 1-53 <BR2>
A; Note: splice form 1
A; Accession: S03592
troponin T, fast skeletal muscle C; Species: Rattus norvegicus (No)
                                                                      A24824
                                                                                                   RESULT 15
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A; Residues: 56-136 < PUT>
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A; Accession: S03591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reywords: acetylated amino end; alternative splicing; differentiation; muscle contract; 1-266/Product: troponin T, fast skeletal muscle splice form 1 *status experimental <w.;1-21.39-266/Product: troponin T, fast skeletal muscle splice form 3 *status experiment; 1-10,17-266/Product: troponin T, fast skeletal muscle splice form 2 *status experiment; 1-10,17-266/Product: troponin T, fast skeletal muscle splice form 2 *status experiment; 1-10,17-266/Product: troponin T, fast skeletal muscle splice form 2 *status experiment. //wodified site: acetylated amino end (Ser) *status experimental
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troponin T, fast skeletal muscle splice form
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63.6%;
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Pred. No. 8.7;
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of troponin
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                                                                                                                                      A;Introns: 6/2; 11/1 17/1; 23/1; 28/1; 32/1; 37/1; 43/2; 58/3; 97/3; 123/. C;Superfamily: troponin T
C;Keywords: alternative splicing; muscle; phosphoprotein; skeletal muscle
                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-272 <BRE>
                                                                                                                                                                                                                                                             A;Title: Complete nucleotide sequence of the fast skeletal troponin T gene. A;Reference number: A24824; MUID:86281691; PMID:3735424 A;Accession: A24824
                                                                                                                                                                                                                                                                                                                   R;Breitbart, R.E.; Nadal-Ginard, J. Mol. Biol. 188, 313-324, 1986
                                                                                                                                                                                                                                                                                                                                                   C;Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Feb-1997 C;Accession: A24824
                                                                                                                                                                                                        C; Genetics:
                                                                                         Query Match
Best Local 9
                                                                          Matches
103
                                     1 ERAEQQRLKSQ 11
ERAEQORIRAE
                                                                      Similarity 7; Conserv
                                                                          Conservative
113
                                                                                         66.1%;
63.6%;
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                                                                                         Score 41;
Pred. No.
                                                                          Mismatches
                                                                                                           DB 2;
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                                                                                                           Length 272;
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                                                                      Gaps
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Search completed: March 13, 2003, 18:53:00 Job time: 13.7636 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Perfect score:
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1 ERAEQQRLKSQDL
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    Issued_Patents_AA: *
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/BCTUS_COMB.pep:*
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US-08-365-103B-14
US-08-365-103B-10
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US-08-602-941-3
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US-08-961-253-521-20
US-09-535-521-20
US-09-535-521-2
US-08-967-2
US-08-967-2
US-08-973-275-1
US-08-973-275-1
US-08-985-103B-6
US-08-365-103B-6
US-09-365-103B-6
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              Sequence 14, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 3, Appli
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Sequence 6, Appli
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Sequence 2, Appli
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                                                                                                                 Query Match
Best Local S
Matches 12
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MOLECULE TYPE:
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ZIP: 50309
                                                                                                                                                                                                                                                                                                      LENGTH:
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                          RAEQQRLKSQDL
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12; Conserv
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34	34	34	34	34	3 4	34	34	34	34	34	υ 4	34	34	34	34	34	34
54.8	54.8	54.8	54.8	54.8	54.8	54.8	54.8	54.8	54.8	54.8	54.8		54.8		54.8		54.8
1248	1248	872	872	872	872	872	872	872	840	724	724	724	431	431	431	362	362
4	N	4	4	4	4	4	w	w	4	4	4	4	4	4	w	4	Ν
US-09-323-735-2	US-09-080-897-2	US-09-430-323-54	US-09-430-323-8	US-08-854-050-54	US-08-854-050-8	US-08-974-549A-221	US-08-851-843A-54	US-08-851-843A-8	US-08-974-549A-190	US-09-562-737-29	US-09-562-737-24	US-09-562-737-21	US-09-553-427-2	US-09-128-275A-2	US-08-478-507-2	US-09-323-735-6	US-09-080-897-6
Sequence 2, Appli	Sequence 2, Appli	Sequence 54, Appl	Sequence 8, Appli	Sequence 54, Appl	Sequence 8, Appli	Sequence 221, App	Sequence 54, Appl	Sequence 8, Appli	Sequence 190, App	Sequence 29, Appl	Sequence 24, Appl	Sequence 21, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 6, Appli	Sequence 6, Appli

ALIGNMENTS

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APPLICANT: Lynch, Richard G
APPLICANT: Nunez, Raphael D.
APPLICANT: Yodoi, Jungi
TITLE OF INVENTION: DNA Sequences for Soluble Froms of CD23
TITLE OF INVENTION: and Methods of Use for Same
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zarley, McKee, Thomte, Voorhees & Sease
STREET: 801 Grand Ave. Suite 3200
CITY: Des Moines
STATE: Iowa
                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Nebel, Heidi S.
REGISTRATION NUMBER: 37,719
REFERENCE/DOCKET NUMBER: Uirf
TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 288-3667
TELEPAX: (515) 288-1338
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14, Application US/08365103B Patent No. 5766943 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
FILING DATE: 28-DEC-
CLASSIFICATION: 435
RAEQQRLKSQDL 13
                                                                                                                                                                                        166 amino acids
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                                       Conservative
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                               91.9%; occ
100.0%; Pr
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                                                      Score 57;
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                                       Mismatches
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0.015;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local Similarity 100.0%; Pred. No
Matches 12; Conservative 0; Mismatc
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                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (515) 288-13: INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                   NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                    TITLE OF INVENTION: DNA Sequences for Soluble Froms of CD23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 167 amino acid
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: and Methods of Use for Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lynch, Rich
APPLICANT: Nunez, Raph
APPLICANT: Yodoi, Jung
                                                                                                                                                                                                                                            APPLICANT: Nunez, APPLICANT: Yodoi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (515) 288-3667 TELEFAX: (515) 288-1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: NEDEL, Heldl S.
REGISTRATION NUMBER: 37,719
REFERENCE/DOCKET NUMBER: UI:
                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                           STREET: 801 Grand
CITY: Des Moines
                                                                                                                                                                                                                                                                                                                                                                                                                                 58 RAEQQRLKSQDL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0 FILING DATE: 28-DEC-1994 CLASSIFICATION: 435
                                                                           COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                               E: Zarley, McKee, Thomte, Voorhees & Sease
801 Grand Ave. Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Zarley, McKee, Thomte, Voorhees & Sease 801 Grand Ave. Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167 amino acids
                                                                                                                                                                                                                                          Lynch, Richard G
Nunez, Raphael D.
Yodoi, Jungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               United States
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Raphael D.
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0.015;
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US-08-365-103B-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/08365103B Patent No. 5766943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, v
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,103B
FILING DATE: 28-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Nebel, Held1 S.
REGISTRATION NUMBER: 37,719
REFERENCE/DOCKET NUMBER: 01rf N5-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Lynch, Richard G
APPLICANT: Nunez, Raphael D.
APPLICANT: Yodo1, Jungi
TITLE OF INVENTION: DNA Sequences for Soluble Froms of CD23
TITLE OF INVENTION: and Methods of Use for Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                         TELEFAX: (515) 288-13: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                        TELEPHONE: (515) 288-3667
TOPOLOGY: 11
                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-D
SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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NAME: Nebel, Heldi S.
REGISTRATION NUMBER: 37,719
REFERENCE/DOCKET NUMBER: Uil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95 RAEQQRLKSQDL 106
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                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Des Moines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
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                                                  LENGTH:
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801 Grand Ave. Suite 3200
                                                    321 amino acids
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n Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                       Release #1.0, Version #1.25
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Query Match

91.9%;

Score 57;

DB 1;

Length 321;

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RESULT 6
US-08-961-264-3
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Sequence 3, Application US/08961264 Patent No. 6025331 GENERAL INFORMATION:
                                                                                                                                                                         Query Match
Best Local :
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Matches 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         quence 3, Application US/08602941 tent No. 5837680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/602,941
FILING DATE: 16-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                               NAME/KEY: Peptide LOCATION: 1.258 OTHER INFORMATION: OTHER INFORMATION:
                                                                                                 102 ERAEQORIRAE 112
                                                                                                                                                          Local Similarity hes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,452
REFERENCE/DOCKET NUMBER: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
SOFTWARE: FastSE(
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                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sir
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Troponin T
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Pred. No. 10;
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US-09-442-099A-3
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Best Local
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TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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MEDIUM TYPE: Diskett
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LOCATION:
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10036-2711
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Sequence 3, Application US/09442099A
Patent No. 6465431
GENERAL INFORMATION:
APPLICANT: Thorn, R.
APPLICANT: Lanser, M.
APPLICANT: Wiederschain, D.
APPLICANT: Wiederschain, D.
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING TROPONIN SUBUNITS,
TITLE OF INVENTION: TRAGMENTS AND HOMOLOGS THEREOF AND METHODS OF THEIR USE TO
TITLE OF INVENTION: INHIBIT ANGIGENESIS
FILE REFERENCE: 8657-028
CURRENT APPLICATION NUMBER: US/09/442,099A
CURRENT FILING DATE: 1997-11-17
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APPLICATION NUMBER: 08/60
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: POISSANT, Brian M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
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1155 Avenue of the Americas
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Sytkowski, Arthur
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Langer, Robert S
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COMPRISING TROPONIN SUBUNITS, FRAGMENTS AND ANALOGS
THEREOF AND METHODS OF THEIR USE TO INHIBIT ANGIOGE
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Pred. No. 10;
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PRIOR FILLING DATE: 1996-02-16
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 3
DENCTH: 258
                                                                                   Query Match
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                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 09/268,274
PRIOR FILING DATE: 1999-03-15
PRIOR APPLICATION NUMBER: 08/961,264
PRIOR FILING DATE: 1997-10-30
PRIOR FILING DATE: 1997-10-30
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Liu, Shigui
APPLICANT: Shi, Qinwei
TITLE OF INVENTION: STABLE TROPONIN SUBUNITS AND COMPLEXES
NUMBER OF SEQUENCES: 6
CORRESSOONDENCE ADDRESS:
                                                                                                                                           TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1112-1-044 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
133
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                                                      Local Similarity nes 7; Conserv
                                                                                                                                                         STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                 TELEPHONE: 201-4-1684
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OPERATING SYSTEM: PC-DOS/MS-DOS
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               1 ERAEQQRLKSQ 11
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TATE: New Jersey
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411 Hackensack Avenue, 4th Floor
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63.6%;
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                                                                     Score 41;
Pred. No.
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Pred. No.
                                                        Mismatches
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; TOPOLOGY: 11r;
; MOLECULE TYPE:
; HYPOTHETICAL: N
US-09-089-593-6
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Best Local Similarity
"---hes 7; Conserve
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US-08-950-925-4
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US-09-089-593-6
                                                                                                                                                        Sequence 4, Application US/08950925
Patent No. 6072040
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                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION: NAME: Jackson Esq., Davi
                                                                                            APPLICANT: Dave, Kirti I.
APPLICANT: Botyanszki, Janos
APPLICANT: Sintar, Eva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 201-487-5800
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Liu, Shigui
APPLICANT: Shi, Qinwei
TITLE OF INVENTION: STABLE TROPONIN SUBUNITS AND COMPLEXES
                             CORRESPONDENCE ADDRESS
                                                               TITLE OF INVENTION:
                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELLERAX: 202
TELLERAX: 133521
                                                                                                                                                                                                                                                     133 ERAEQQRIRNE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: Zui-vo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1112-1-044 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/089,593 FILING DATE:
ADDRESSEE: MORRISON & FOERSTER STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Hackensack
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                                                                                                                                                                                                                                                                       1 ERAEQQRLKSQ 11
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5. 6060278
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                                                             Stabilized Conjugates of Uncomplexed Subunits of Multimeric Proteins
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Pred. No. 11;
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STATE:

Palo Alto CA

COMPUTER READABLE FORM:

94304-1018

COUNTRY:

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                                                                                                                        ; ORGANISM: Canis familiaris US-09-535-521-20
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                      SEQ ID NO 20
LENGTH: 208
                                                                                                                                                                                                                                                                                                                                                                        Sequence 20, Application US/09535521 Patent No. 6410714 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                              Matches
                                                                                         Query Match
                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/535,521
CURRENT FILING DATE: 2000-03-24
EARLIER APPLICATION NUMBER: 60/125,913
EARLIER FILING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                                                                                                           APPLICANT: Weber, Eric R.
APPLICANT: McCall, Catherine A.
TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY 19E RECEPTOR (CANINE CD23)
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
FILE REFERENCE: AL-5
                                                                                                                                                                                                   SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATE:
FILING DATE:
FILING DATE:
ATTORNEY/ACENT INFORMATION:
NAME: Axford, Laurie A
NAME: Axford, Laurie A
35,053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/950,925
FILING DATE:
CLASSIFICATION: 530
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FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 35,053
REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 ERAEQORIRNE 143
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TELEFAX: 706141
 16
                                                                            Local
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                            2 RAEQQRLKSQD 12
QAEQKRMKAQD
                                                            Similarity 63.07; Conservative
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Pred. No.
                                                                         Score 40; DB
Pred. No. 12;
                                                            Mismatches
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                                                                                         Length 208
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RESULT 12

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APPLICANT: Weber, Eric R.

APPLICANT: McCall, Catherine A.

APPLICANT: MCCall, Catherine A.

TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)

TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF

FILE REFERENCE: AL-5

CURRENT FILING LATE: 2000-03-24

CURRENT FILING LATE: 2000-03-24

EARLIER APPLICATION NUMBER: 60/125,913

EARLIER APPLICATION NUMBER: 60/125,913

EARLIER FILING DATE: 1999-03-24

NUMBER OF SEQ ID NOS: 26

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 5

LENGTH: 292

TYPE: PRT

ORGANISM: Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 292
; TYPB: PRT
; ORGANISM: Canis familiaris
US-09-535-521-2
                                                                                                                                                                                            RESULT 14
US-08-986-967-2
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                                                                                                                                                        Patent No. H00202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                      Sequence
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Best Local
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                GENERAL INFORMATION:
APPLICANT: Hoskins, Jo A.
APPLICANT: Jaskunas Jr., Stanley R.
APPLICANT: Rockey, Pamela K.
APPLICANT: Treadway, Patti J.
TITLE OF INVENTION: Streptococcus Pneumoniae Gene Sequence
TITLE OF INVENTION: GIPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Weber, Eric R.
APPLICANT: McCall, Catherine A.
APPLICANT: MCCall, Catherine A.
TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
FILE REFERENCE: AL-5
CURRENT APPLICATION NUMBER: US/09/535,521
CURRENT FILING DATE: 2000-03-24
EARLIER APPLICATION NUMBER: 60/125,913
EARLIER FILING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 26
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                      100 QAEQKRMKAQD 110
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GrpE
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63.6%;
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Pred. No.
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Pred. No.
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; LENGTH: 174 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-986-967-2
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 6348328 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/986,967
FILING DATE: US/08/986,967
CLASSIFICATION: 536
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                     APPLICANT: Nicholas, Richard
APPLICANT: Stodola, Robert
TITLE OF INVENTION: No. 6348328el Compounds
NUMBER OF SEQUENCES: 552
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
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                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                               COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 317-276-3334
TELEFAX: 317-276-2763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: x-11756
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ADDRESSEE: E11 Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Black, Michael APPLICANT: Hodgson, John
                                                                             APPLICATION NUMBER: US/08/858,207A FILING DATE: 09-MAY-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
                                                                                                                                                                                                                                                                                             STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 59.7%;
Local Similarity 61.5%;
les 8; Conservative
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: 46285
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Knowles, David
Nicholas, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37;
Pred. No.
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31;
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; MOLECULE TYPE: NO. 6348328e
US-08-858-207A-293
Search completed: March 13, 2003, 18:53:53 Job time : 12.5818 secs
                                                             밁
                                                                                                                   Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 174 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                          63 ERONLORYRSODL 75
                                                                                                                                                                                                                                                                                                                        TELEFAX: 610-270-5090
                                                                               1 ERAEQORLKSODL 13
                                                                                                                        Conservative
                                                                                                                                     59.7%;
                                                                                                                                      Score 37;
Pred. No.
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Q1-CCT-2000
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SEQUENCE
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SEQUENCE FROM N.A. STRAIN-FIN92168; Liitsola K., Holmstrom P., Laukkanen T., Brummer-Korvenkonti Leinikki P., Salminen M.O.; Analysis of HIV-1 genetlc subtypes in Finland reveals good "Analysis of HIV-1 genetlc subtypes in Finland reveals good "Topic Topic To Viruses; Retroid viruses; Retroviridae; NCBI_TaxID-11676; Human immunodeficiency virus type (TTEMBLrel. 15, Created) (TTEMBLrel. 15, Last sequence update) (TTEMBLrel. 15, Last annotation update) (Fragment). Created) Last sequence update) Score 40; Pred. No. 7F85C2C145AF1677 CRC64; PRT; PRT; Mismatches T., Brummer-Korvenkontio 54 46 DB 15; 0.89; Lentivirus ₹ ₹ 0; Length 46 Indels 0 Η., Gaps

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RESULT
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Leinikki P., Salminen M.O.;
"Analysis of HIV-1 genetic subtypes in
correlation between molecular and epide
Scand. J. Infect. Dis. 0:0-0(2000).
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Pfam; PF00098; zf-CCHC; 1.
SMART; SM00343; znf_C2HC; 1.
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EMBL; AF21933; AAF30239.1; -.
HSSP; P05888; 1AAF.
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NCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus
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Viruses; Retroviridae;
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nilarity 100.0%;
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Best Local Similarity
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Best Local
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Q9J144;
Q1-OCT-2000
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01-MAR-2002
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01-OCT-2000
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NON_TER
SEQUENCE
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Liitsola K., Holmstrom P., Laukkanen T., Desumment Leinikki P., Salminen M.O.;

Leinikki P., Salminen M.O.;

"Analysis of HIV-1 genetic subtypes in Finland reveals good correlation between molecular and epidemiological data.";

"Analysis of HIV-1 genetic subtypes in Finland reveals good correlation between molecular and epidemiological data.";
                                                                                                                   NON_TER
                                                                                                                                                                                                                             correlation between molecular Scand. J. Infect. Dis. 0:0-0(2 EMBL; AF219329; AAF30235.1; -. HSSP; P05888; 1AAF.
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Viruses; Retroid viruses; Retroviridae;
NCBI_TaxID=11676;
                                                                                              SEQUENCE
                                                                                                                                                           Pfam; PF00098; zf-CCHC; 1.
SMART; SM00343; ZnF_C2HC; 1.
                                                                                                                                                                                                                                                                                                                  Liitsola K., Holmstrom P., Laukkanen T.
Leinikki P., Salminen M.O.;
"Analysis of HIV-1 genetic subtypes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae;
NCBI_TaxID=11676;
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EMBL; AF219356; AAF30262.1;
HSSP; PO5888; IAAF.
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                                                                                                                                                                                                             InterPro; IPR001878; Znf_CCHC.
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6191 MW;
                                                                                           6414 MW;
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88.9%; Score 40; DB
100.0%; Pred. No. 1.
Live 0; Mismatches
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Pred. No.
                                                                                           86B45037A48AE958 CRC64
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                                               DB 15; Length 58
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RESULT
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Matches 9
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Best Local Similarity 100

Matches 9; Conservative
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01-OCT-2000
01-MAR-2002
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Q9J198;
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SEQUENCE
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"Analysis of HIV-1 genetic subtypes in Finland reveals correlation between molecular and epidemiological data. Scand. J. Infect. Dis. 0:0-0(2000).
SCANDL AFF. 19335; AARF0241.1;
HSSP: P05888; 10AF.
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01-OCT-2000
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Leinikki P., Salminen M.O.;
"Analysis of HIV-1 genetic subtypes in
correlation between molecular and epide
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SMART; SM00343; ZnF_C2HC;
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SMART; SM00343; ZnF_C2HC; 1.
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| KARVLAEAM
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                                                                                       Similarity
9; Conser
                                                                                                                                                                                                           61
61 AA;
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8 AA;
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                                                                                    Score 40; DB; Pred. No. 1.2
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Pred. No.
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                                                                                                                                               DB 15; Length 61;
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Q9J168;
01-OCT-2000
01-OCT-2000
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09J197;
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SMART; SM00343; ZnF_C2HC; 1.
NON_TER 1 1
                                                                                                                                                             InterPro; IPR001878; znf_CCHC. Pfam; PF00098; zf-CCHC; 1.
                                                                                                                                                                                                    Scand. J. Infect. Dis. 0:0-0(2
EMBL; AF219305; AAF30211.1; -
HSSP; P05888; 1AAF.
                                                                                                                                                                                                                                                              Leinikki P., Salminen M.O.; "Analysis of HIV-1 genetic subtypes in Finland reveals good correlation between molecular and epidemiological data.";
                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; Retroid viruses; NCBI_TaxID=11676;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-FIN93180;
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                                                                                      SEQUENCE
                                                                                                                                           SMART; SM00343; ZnF_C2HC; 1.
                                                                                                                                                                                                                                                                                                                                           STRAIN-FIN9213;
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Leinikki P., Salminen M.O.;
                                                                                                                                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
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6924 MW;
88.9%; 5u
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Retroviridae;
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097612;

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01-DEC-2001 (TrEMBLrel. 1:

01-MAR-2002 (TrEMBLrel. 2:
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09J132;
01-OCT-2000
01-OCT-2000
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Gag protein
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                                                                                   InterPro; IPR001878; znf_CCHC. Pfam; PF00098; zf-CCHC; 1. SMART; SM00343; znf_C2HC; 1.
                                                                                                                                                                                                                                                                                                                                         STRAIN-RUS9419;
Liitsola K., Laukkanen T., Denis
Smolskaja T., Ustina V., Vlasov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus type 1. Viruses; Retroid viruses; Retroviridae; RCBI_TaxID=11676;
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LiltSola K., Holmstrom P., Laukkanen T.
Leinikki P., Salminen M.O.;
"Analysis of HIV-1 genetic subtypes in
"Analysis of HIV-1 molecular and epide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPRO01878; znf_CCHC. pfam; pr00098; zf-CCHC; 1. SMART; SM00343; znf_C2HC; 1.
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Smolskaja T., Ustina V., Vlasov N.,
"Genetic characterization of HIV-1:
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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Leinikki P., Salminen M.;
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RESULT 13
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          Liitsola K., Holmstrom P., Laukkanen T.,
Leinikki P., Salminen M.O.;
"analysis of HIV-1 genetic subtypes in Fi
correlation between molecular and epidem1
Scand. J. Infect. Dis. 0:0-0(2000).
EMBL; AF219347; AAF30253.1; -.
HSSP; P05888; 1AAF.
InterPro; IPR001878; 2nf_CCHC.
pfam; PF00098; zf-CCHC; 1.
SMARR; SM00343; ZnF_C2HC; 1.
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Leinikki P., Salminen M.O.;
Analysis of HIV-1 genetic subtypes in Finland reveals
Correlation between molecular and epidemiological data.
Correlation between molecular and epidemiological data.
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Gag protein
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Viruses; Retroid viruses; Retroviridae;
NCBL_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae;
NCBI_TaxID=11676;
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InterPro; IPR001878; Znf_CCHC.
Pfam; PF00098; zf-CCHC; 1.
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Q9J123;
          Liitsola K., Holmstrom P., Laukkanen T., Brummer-Korvenkontio H., Leinikki P., Salminen M.O.;
"Analysis of HIV-1 genetic subtypes in Finland reveals good correlation between molecular and epidemiological data.";
Scand. J. Infect. Dis. 0:0-0(2000).
EMBL; AF19284; AAF30190.1; -.
HSSP; P05888; laAF.
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Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID-11676;
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EMBL; AF219350; AAF30256.1; -.
HSSP; P05888; IPR01878; Znf_CCHC.
Pfam; PF00098; Zf-CCHC; 1.
SMART; SM00343; ZnF_C2HC; 1.
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Leinikki P., Salminen M.O.;
"Analysis of HIV-1 genetic subtypes in F
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B1298 IA. \$\text{\$\text{\$\text{\$WMJ2}\$}} 721; 071; 071; ag_p; in; p 13 36 36 37 >38	entry ss In infor fit s sta s a l to l	for AIDS."; 232.1548-1553(19 232.1548-1553(19 232.1548-1553(19 EMBLY, BUDDING, M LICATION CYCLE. D BRANE ASSOCIATION ULT IN BUDDING OF PRECURSORS ALSO D AND PACKAGE TWO CELLANEOUS: ISOLA OD SAMPLES SEQUEN PERINATALLY INFE	ien vir vir Pu .M.	ANDA 09, 28, 40, Cont		ប្រហាធាធាធាធាធាធាធាធាធាធាធាធាធាធាធាធាធាធាធ
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Best Local s
Matches
                                                                                                              EMBL; M62320; AAA75018.1; -.
HSSP; P05888; IAAF.
InterPro; IPR000721; Gag_p24.
InterPro; IPR000071; Retrovir_p17.
InterPro; IPR000078; Znf_CCHC.
Pfam; PF000098; Zf-CCHC; 2.
Pfam; PF000540; Gag_p17; 1.
Pfam; PF00540; Gag_p24; 1.
Pfam; PF00599; CaHCZNFINGER.
PRINTS; PR00539; C3HCZNFINGER.
PRINTS; PR00234; HIVIMATRIX.
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P24736;
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SEQUENCE
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01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
AAG polyprotein (Contains: Core proteins P17,
                                                                                                                                                                                                                                                                              This
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ZN_FING
                                                                          AIDS; Core pi
Zinc-finger;
                                                                                                       SMART; SM00343;
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MEDLINE=91090981; PubMed=2265025;
MEDLINE=91090981; PubMed=2265025;
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NCBI_TaxID=11703;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HIV-1).
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PTM: THE P24 PROTEIN IS PHOSPHORYLATED.

SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
                                                                                                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through a collab
ween the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
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9; Conservative
                                                                                             M00343; ZnF_C2HC; 2
PS50158; ZF_CCHC; :
                                                                                   protein;
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43314 MW;
                                                                                    Polyprotein;
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       BY SIMILARITY.
CORE PROTEIN P1
CORE PROTEIN P2
CORE PROTEIN P2
CORE PROTEIN P7
CORE PROTEIN P1
CORE PROTEIN P1
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Pred. No.
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                                                                                   Myristate; Phosphorylation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lentivirus
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         P17
N P24
N P2.
N P7
N P1.
N P6.
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                           (NUCLEOCAPSID PROTEIN)
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                                              (CORE ANTIGEN).
                                                       (MATRIX PROTEIN)
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Query Match
Best Local :
                                                                                                     InterPro; IPR000721; Gag_p24.
InterPro; IPR000721; Retrovir_p17.
InterPro; IPR00078; Znf_CCHC.
Pfam; PF00098; Zf-CCHC; 2.
Pfam; PF00540; Gag_p17: 1.
Pfam; PF00607; Gag_p24: 1.
Pfam; PF00607; Gag_p24: 1.
PRINTS; PR00234; HIVIMATRIX.
PRINTS; PR00234; HIVIMATRIX.
SMART; SM00343; ZnF_CCHC; 2.
PROSITE; PS50158; ZF_CCHC; 2.
Zinc-finger;
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P18800;
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LIPID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                        AIDS; Core
                                                                                                                                                                                                                                                                                                                 EMBL; M27323; AAA44868.1;
PIR; JQ0065; FOLJND.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1990 (Rel. 16, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
GAG polyprotein (Contains: Core proteins Pl
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HIV; M27323; GAG$NDK.
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Hampe A., Chermann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; Retroid
NCBI_TaxID=11695;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleotide sequence of HIV1-NDK:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           354 KARVLAEAM 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL ASSEMBLY, THE PROTEINS FORM MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL. GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA. PTM: THE P24 PROTEIN IS PHOSPHORYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MISCELLANEOUS: NDK, ISOLATED FROM A ZAIRIAN PATIENT AIDS, AND IS A HIGHLY CYTOPATHOGENIC STRAIN. SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
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sen the Swiss Institute of Bioinformatics and the EM
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 128
359
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J.C.;
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                                                                                    Polyprotein;
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BY SIMILARITY.

CORE PROTEIN P17

CORE PROTEIN P24

CORE PROTEIN P2.
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Pred. No.
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MYRISTATE (BY SIMILARITY).
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                                                                                      Phosphorylation;
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                   (MATRIX PROTEIN).
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Best Local 9
                                                                                              Pfam; PF00098; zf-CCHC; 2.
Pfam; PF00540; Gag_P17; 1.
Pfam; PF00540; Gag_P24; 1.
Pfam; PF00607; Gag_P24; 1.
PRINTS; PR00939; C2HCZNFINGER.
PRINTS; PR00939; C2HCZNFINGER.
PROSITE; PS50158; ZF_CCHC; 2.
PROSITE; PS50158; ZF_CCHC; 2.
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01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
GAG polyprotein [Contains: Core proteins P17,
     INIT_MET
                                                                                                                                                                                                                                                                                  InterPro; IPR000721; Gag_p24.
InterPro; IPR000071; Retrovir_p17.
InterPro; IPR001878; Znf_CCHC.
                                                                                                                                                                                                                                                                                                                                                                EMBL; M26727; AAA83391.1;
HSSP; P05888; 1AAF.
HIV; M26727; GAG$OYI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Huet T., Dazza M.C., Brun-Vezinet F., Roelants G. "A highly defective HIV-1 strain isolated from a individual presenting an atypical western blot."; AIDS 3:707-715(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immunodeficiency virus type 1 (OYI isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=11699;
                                                   AIDS; Core protein; Polyprotein; Myristate; Zinc-finger; Repeat.
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PTM: THE P24 PROTEIN IS PHOSPHORYLATED.

MISCELLANEOUS: THE OUT INSULATE WAS TAKEN FROM THE BLOOD OF A MISCELLANEOUS: THE OUT INSULATE WAS TAKEN FROM THE BLOOD OF A
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Pred. No.
BY SIMILARITY.
CORE PROTEIN P17
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                                                                           Phosphorylation;
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PIR; A2553; FOVWH4.

HSSP; P0588; IAAF.

HIV; M13136; GAGSCDC45.

InterPro; IPR000721; Gag_p24.

InterPro; IPR00071; Retrovir_p17.

InterPro; IPR001878; Znf_CCHC.

Pfam; PF00098; Zf-CCHC; 2.

Pfam; PF00540; Gag_p17; 1.

Pfam; PF00540; Gag_p247; 1.

PFAM; PF00540; Gag_p247; 1.

PRINTS; PR00939; C2HCXNFINGER.

PRINTS; PR00234; HIVIMATRIX.

SMART; SM00343; ZnF_CCHC; 2.

PROSTTE; PS50158; ZF_CCHC; 2.

AIDS; Core protein; Polyprotein; Myr

Myristate; Phosphorylation;

EMBL;

M13136; AAA44306.1;

or send an email to license@isb-sib.ch).

requires a

license agreement (See

http://www.isb-sib.ch/announce/

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GAG_HOAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       divergence in its genomic sequences.";

Proc. Natl. Acad. Sci. U.S.A. 83:8380-8384(1986).

Proc. Natl. Acad. Sci. U.S.A. 83:8380-8384(1986).

Froc. Natl. Acad. Sci. U.S.A. 83:8380-8384(1986).

FOUNTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE PROTEINS FORM ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAMELY MEMBRANE ASSOCIATIONS AND SELET-ASSOCIATIONS THAT ULTIMATELY RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL.

GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVE GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVE BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.

-!- PIM: THE P24 PROTEIN IS PHOSPHORYLATED.

-!- SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
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01-FEB-1994 (Rel. 28, Last
15-JUN-2002 (Rel. 41, Last
GAG polyprotein [Contains:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-87041461; PubMed-3490666;
Desai S.M., Kalyanaraman V.S., Casey J.M., Srinivasan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Molecular cloning and primary nucleotide sequence analysis of a distinct human immunodeficiency virus isolate reveal significant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Molecular cloning and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Andersen P.R., Devare S.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; Retroid
NCBI_TaxID=11687;
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Core proteins P17,
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GAG_HV1EL
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HSSP; PODBBB; IT...

HIV; KO3454; GAGSELL.

Interpro; IRR000721; Gag_p24.

Interpro; IPR000771; Retrovir_p17.

Interpro; IPR001878; Znf_CCHC.

Pfam; PF00098; Zf-CCHC; 2.

Pfam; PF00540; Gag_p17; 1.

R Pfam; PF00607; Gag_p24; 1.

R Pfam; PF00607; Gag_p24; 1.

R Pfam; PF00343; Znf_CZHCZ; 2.

NR PRINTS; PR00343; Znf_CZHC; 2.
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Best Local
                                                                                                                                                                                                                                                            EMBL; K03454;
EMBL; A07108;
HSSP; P05888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "BLULINE=86245056; PubMed=2424612; Alizon M., Wain-Hobson S., Montagnier L., "Genetic variability of the AIDS virus: no of two isolates from African patients."; Cell 46:63-74(1986).
                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-slb.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-AUG-1987 (Rel. 05, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
GAG polyprotein (Contains: Core proteins p17, p24, p2, p7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZN_FING
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CHAIN
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NCBI_TaxID=11689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus type 1 (ELI isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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INIT_MET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA. PTM: THE P24 PROTEIN IS PHOSPHORYLATED. SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL. GAGG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KARVLAEAM 366
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CAA00611.1; -.
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CORE PROTEIN P.
CCHC-TYPE 2.
MYRISTATE (BY
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Pred. No.
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E PROTEIN P24
E PROTEIN P2.
E PROTEIN P7 (
E PROTEIN P1.
E PROTEIN P6.
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RESULT 7
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Best Local :
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01-FEB-1994
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAG_HV1H2
P04591;
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                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by ancentities requires a license agreement (See http://www.isb-sentities requires a license agreement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                      InterPro; IPR000721; Gag_p24.
InterPro; IPR000071; Retrovir_p17.
InterPro; IPR001878; Znf_CCHC.
Pfam; PF00098; zf-CCHC; 2.
                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                        AIDS
                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-87299196; PubMed-3040055;
Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H.,
Gallo R.C., Wong-Staal F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUN-2002 (Rel. 41, Last annotation update) GAG polyprotein [Contains: Core proteins P17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AIDS; Core p.
Zinc-finger;
                                                                                                     HIV; K03455; GAG$HXB2.
                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                    virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses;
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                                                                                                                 HSSP;
                                                                                                                                                                                                                                                                                                                                                                             *Complete nucleotide sequences of functional
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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                                                                                                                                                                                                                                         IS RES. Hum. Retroviruses 3:57-69(1987).

S RES. Hum. RETRORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE VIRAL ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL ASSEMBLY, THE PROTEINS FORM REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL. GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.

PTM: THE P24 PROTEIN IS PHOSPHORYLATED.

SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KARVLAEAM 366
                                                                                                               P05888; 1AAF.
                                                                                                                           K03455; AAB50258.1;
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9; Conser
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(Rel. 28, Last sequence up)
(Rel. 41, Last annotation
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390
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Pred. No.
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8A1785A59EAED08D CRC64;
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RESULT 8
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                 HIV; M21137; GAGSJH3.

InterPro; IPR000721; Gag_p24.

InterPro; IPR000071; Retrovir_p1

InterPro; IPR001878; Znf_CCHC.

Pfam; PF00098; zf-CCHC; Z.

Pfam; PF00540; Gag_p17; 1.

Pfam; PF00540; Gag_p24; 1.

PRINTS; PR00939; C2HCZNFINCER.

PRINTS; PR00234; HIVIMATRIX.
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01-OCT-1989 (
01-FEB-1994 (
15-JUN-2002 (
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ZN_FING
LIPID
                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                Komiyama N., Hattori N., Inoue J., Sakuma S., Kurimura T., Yoshida M., "Nucleotide sequences of gag and env genes of a Japanese isolate of HIV-1 and their expression in bacteria.",

AIDS Res. Hum. Retroviruses 5:411-419(1999).

-1- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL REPLICATION OYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL. GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.

-1- PTM: THE P24 PROTEIN IS PHOSPHORYLATED.

-1- SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zinc-finger;
INIT_MET
                                                                                                                  EMBL; M21137; AAB03522.1; HSSP; P05888; 1AAF.
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus type 1 (JH3 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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(Rel. 41, Last annotation
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                                                                       Retrovir_p17.
2nf_CCHC.
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Pred. No.
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MYRISTATE (BY SIMILARITY).
774C384D6EACB108 CRC64;
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PROTEIN P24
PROTEIN P2.
PROTEIN P7 (
PROTEIN P1.
PROTEIN P1.
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Pfam; Provoc.; PRO0399; C2HCZNF INC...
PRINTS; PRO0234; HIV1MATRIX.
PRINTS; PRO02343; ZnF_C2HC; 2.
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between
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                            Pfam; PF00098; zf-CCHC; 2.
Pfam; PF000540; Gag_p11; 1.
Pfam; PF00607; Gag_p24; 1.
PRINTS; PR00939; C2HCZNFINGER.
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GAG_HV1LW
Q70622;
15-JUL-1998 (
15-JUL-1998 (
15-JUN-2002 (
                                                                                                                                                                                                                                                                                                                                                  "Viral variability and serum antibody response in a laboratory worker infected with HIV type 1 (HTLV type IIIB).";
AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
AIDS Res. Hum. PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM MEMBRANE ASSOCIATIONS AND SELET-ASSOCIATIONS THAT ULTIMATELY RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL. GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY
                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reitz M.S. Jr., Hall L., Robert-Guroff M., Shaw G.M., Kong L.I., Weiss S.H., Waters D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zinc-finger;
InterPro; IPR000721; Gag_p24.
InterPro; IPR000071; Retrovir_p17.
InterPro; IPR001878; Znf_CCHC.
                                                            EMBL; U12055; AAA76686.1;
HSSP; P05888; lAAF.
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                                                                                                                                                entities requires a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus type 1 (LW12.3 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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                                                                                                                                                                                                                                                                                        BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA. PTM: THE P24 PROTEIN IS PHOSPHORYLATED. SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
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                                                                                                                           an email to license@isb-sib.ch).
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                                                                                                                                                license agreement (See http://www.isb-sib.ch/announce/
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Pred. No.
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MYRISTATE (BY SIMILARITY)
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    L. Lautenberger J., Hahn B.M.
    D., Gallo R.C., Blattner W.;
    Sponse in a laboratory worker

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Best Local
                                                                                Pfam; PF00098; zf-CCHC; 2.
Pfam; PF00540; Gag_p17; 1.
Pfam; PF00540; Gag_p24; 1.
Pfan; PF00697; Gag_p24; 1.
PRINTS; PR00939; C2HCZNEINGER.
PRINTS; PR00234; HIVIMATRIX.
SMART; SM00343; ZnF_C2HC; 2.
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Zinc-finger;
INIT_MET
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                           SMART; SM00343; znF_C2HC; 2. PROSITE; PS50158; ZF_CCHC; 2 AIDS; Core protein; Polyprot
                                                                                                                                                                                                                                                          InterPro; IPR000721; Gag_p24.
InterPro; IPR000071; Retrovir_p17.
InterPro; IPR001878; Znf_CCHC.
                                                                                                                                                                                                                                                                                                                                                             HIV; M19921; GAG$NL43.
                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M19921; AAA44987.1; HSSP; P05888; 1AAF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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01-0CT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1994
15-JUN-2002
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(Rel. 28, Last sequence (Rel. 41, Last annotation)
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viruses; Retroviridae; Lentivirus.
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                           Polyprotein;
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Pred. No.
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MYRISTATE (BY SIMILARITY).
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tation update)
proteins P17, P24, P2, P7, P1,
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                        Myristate; Phosphorylation;
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E PROTEIN P2.
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E PROTEIN P7.
E PROTEIN P1.
E PROTEIN P6.
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There are no restrictions
ong as its content is in
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HSSP; P05888; IAAR:
InterPro; IPRO00721; Retrovir_p17.
InterPro; IPRO01878; Znf_CCHC.
Pfam; PF0098; Zf-CCHC; 2.
Pfam; PF00540; Gag_p17; 1.
Pfam; PF00540; Gag_p24; 1.
PFANTS; PR00939; C2HCZWFINGER.
PRINTS; PR00934; HIVIMATRIX.
PRINTS; PR00934; AFF_C2HC; 2.
SMART; SM00343; ZnF_C2HC; 2.

PIR; A44001; A44001. HSSP; P05888; lAAF. EMBL; M93258; -; use by non-profit institutions as long modified and this statement is not removed

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-!- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE
                                                                                                                                                                                                                                                                                                                                                                  Shaw G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAG polyprotein
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15-JUN-2002
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                                                                                                                                                                                                                                                                                                                                            properties of human immunodeficiency virus type 1 in
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=93021387; PubMed=1404605;
                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=36377;
                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses;
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                                                                                                                                                                                                                                                                                                                                                       'Complete nucleotide sequence,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 KARVLAEAM 10
                                                                                                                                                                                                                               SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
                                                                                                                                                                                                                                        ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL. GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA. PTM: THE P24 PROTEIN IS PHOSPHORYLATED.
                                                                                                                                                                                                                                                                                                                                   limited defectiveness and complementation.";
                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through 
men the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                            Hui H., Burgess C.J., Price R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
9; Conser
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(Rel. 29, Last sequence update)
(Rel. 41, Last annotation updat
tein [Contains: Core proteins Pl
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Pred. No.
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CORE PROTEIN
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MYRISTATE (BY SIMILARITY)
C8ECC1302FE2C1E2 CRC64;
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Best Local
                                                                                   Pfam; PF00098; zf-CCHC; 2.

Pfam; PF00540; Gag_p17; 1.

Pfam; PF00607; Gag_p24; 1.

PRINTS; PR00939; CZHCZNFINGER.

PRINTS; PR00234; HIV1MATRIX.

SMART; SM00343; ZnF_CZHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P12495;
01-OCT-1989
01-FEB-1994
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (NOV-1988) to the HIV data bank.

-i- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL ASSEMBLY, THE PROTEINS FORM MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY RESULT IN BUDDING OF AN IMMATURE VIRTON FROM THE INFECTED CELL. GAG PRECURSORS ALSO FUNCTION BURING VIRAL ASSEMBLY TO SELECTIVELY BIND AND PACKACE TWO PLUS STRANDS OF GENOMIC RNA.
-i- PTM: THE P24 PROTEIN IS PHOSPHORYLATED.
-i- SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZN_FING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
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                                                                                                                                                                                                              InterPro; IPR000721; Gag_p24.
InterPro; IPR000071; Retrovir_p17.
InterPro; IPR001071; Refrovir_p17.
InterPro; IPR001078; Zaf_CCHC.
Pfam: PF00098; Zaf_CCHC; 2.
                                                                                                                                                                                                                                                                                                           HSSP; P05888; 1AAF.
HIV; M22639; GAG$Z2Z6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immunodeficiency virus type 1 (22/CDC-234 isolate) (HIV-1). Viruses; Retroid viruses; Retroviridae; Lentivirus.
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                   AIDS; Core protein; Polyprotein; Myristate; Phosphorylation; Zinc-finger; Repeat.
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                                                                       PROSITE;
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                                                                       PS50158; ZF_CCHC;
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(Rel. 28, Last sequence update)
(Rel. 41, Last annotation updat
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    41, Last annotation update)
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CORE PROTEIN P24 (CO
CORE PROTEIN P2.
CORE PROTEIN P7 (NUC
CORE PROTEIN P1.
CORE PROTEIN P6.
CCHC-TYPE 1.
CCHC-TYPE 2.
MYRISTATE (BY SIMILA
MY: 278E665F5405CD99 (M)
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RESULT 13
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Best Local
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HIV; K02007; GAGSSF2.
InterPro; IPR000071; Retrovir_p17.
InterPro; IPR001878; Znf_CCHC.
                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
GAG polyprotein [Contains: Core proteins P17,
                                                                                                                                                                                                                                          PIR; A03947; FOVWA2.
HSSP; P05888; 1AAF.
                                                                                                                                                                                                                                                                                       EMBL; K02007; AAB59875.1;
                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ARV-2).";
Science 227:484-492(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Nucleotide sequence and expression of an AIDS-associated retrovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stempien M.M., Brown-Shimer S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=85090453; PubMed=2578227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus type 1 (ARV2/SF2 isolate) (HIV-1). Viruses; Retroid viruses; Retroviridae; Lentivirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM MEMBRANE ASSCCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL. GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA. PTM: THE P24 PROTEIN IS PHOSPHORYLATED.
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J.A., Dina D., Luciw P.A.;
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0; Mismatches
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InterPro; IPROVIDED STATEMENT OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PRINTS; PRO0507; Gag_P24; 1.

PRINTS; PRO0939; C2HCXMFINGER.
PRINTS; PRO0234; HIVIMATRIX.
PRINTS; PRO0343; ZnF_C2HC; 2.

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GAG_H

AC P2087

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Best Local S
Matches 9
                                                                                        EMBL; M38429; AAB03744.1; -.
HSSP; P05888; IAAF.
HIV; M38429; GAGSJRCSF.
HIV; M38429; GAGSJRCSF.
InterPro; IPR0000721; Gag_p24.
InterPro; IPR000071; Retrovir_p17.
InterPro; IPR001878; Znf_CCHC.
Pfam; PF00098; Zf-CCHC; 2.
Pfam; PF000540; Gag_p17: 1.
Pfam; PF00550; Gag_p24: 1.
Pfam; PF000507; Gag_p24: 1.
PFINTS; PR00939; C2HCZNFINER.
PRINTS; PR00934; HIVLMATRIX.
SMART; SM00343; ZnF_CCHC; 2.
PROSTTE; PS50158; ZF_CCHC; 2.
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AIDS; Core protein;
Zinc-finger; Repeat
INIT_MET 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Koyanagi S., Chen I.,
Submitted (DEC-1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immunodeficiency virus type 1 (JRCSF isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Zinc-finger;
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                                                                Polyprotein; Myristate; Phosphorylation;
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Pred. No.
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ORE PROTEIN P17
ORE PROTEIN P24
ORE PROTEIN P2.
ORE PROTEIN P7 (1)
ORE PROTEIN P1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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E (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                 RP SEQUENCE FROM N.A.

MEDLINE-66245056; PubMed=2424612;

RA Alizon M., Wain-Hobson S., Montagnier L., Sonigo P.;

RA Alizon M., Wain-Hobson S., Montagnier L., Sonigo P.;

RRA Alizon M., Wain-Hobson S., Montagnier L., Sonigo P.;

RR Cell 46:63-74(1986).

CC Lei 46:63-74(1986).

CC CLE DESCRIPTION, AND INTECTION STACES OF THE VIRAL SCENBLY, BUDDING, MATURATION, AND INTECTION STACES OF THE VIRAL ASSEMBLY, THE PROTEINS FORM MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT LUTIMATELY RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL.

CC GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY BIDD AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.

CC BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.

CI - PTM: THE P24 PROTEIN IS PHOSPHORYLATED.
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Best Local
       InterPro; IPR000721; Gag_p24.
InterPro; IPR000071; Retrovir_p17.
InterPro; IPR001878; Znf_CCHC.
Pfam; PF00098; zf-CCHC; 2.
Pfam; PF00540; Gag_p217; 1.
Pfam; PF00607; Gag_p24; 1.
Pfam; PF00607; Gag_p24; 1.
PRINTS; PR00939; C2HCZMFINGER.
PRINTS; PR00934; HIVLMATRIX.
SMART; SM00343; ZnF_CCHC; 2.
PROSITE; PS0158; ZF_CCHC; 2.
AIDS; Core protein; Polyprotein; Myr
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13-AUG-1987 (Rel. 05, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
GAG polyprotein [Contains: Core proteins P17,
                                                                                                                                                                   EMBL; X04415; CAA2801
EMBL; A07116; CAA0061
HSSP; P05888; lAAF.
HIV; K03456; GAGSMAL.
                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAG
                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; Retroid
NCBI_TaxID=11697;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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CORE PROTEIN P1 (NUCLEOCAPS: CORE PROTEIN P1.)
CORE PROTEIN P6.
CORE PROTEIN P6.
CCHC-TYPE 1.
CCHC-TYPE 1.
CCHC-TYPE 2.
MYRISTATE (BY SIMILARITY).
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Pred. No.
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                                                                                                                                                                                                                                                                   Usage
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 283224 seqs, 96134422 residues
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Listing first 45 summaries
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$24478
$24478
$29 polyprotein - human immunodeficiency virus type 1 (fragment)
N;Contains: p24 protein; p25 protein; p7 protein
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 20-Feb-1995 #sequence_revision 26-Jul-1996 #text_change 26-Aug-1999
C;Accession: $24478; $24484
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                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, October 1991 A; Reference number: S24471
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PID:g939876

gag polyprotein - gag polyprotein - hypothetical prote	FOLJGG FOLJGG H70725	2-	522	75.6 75.6	34 4	44 £
gag gag	S53091 FOLJG2	- 2	521 522	75.6	ω ω 4-4	
Seb Seb	S12152	NK	521	75.6	34	
gaç	FOLJCA		521	75.6	34	_
pap gag	FOLJST	<u> </u>	510 521	75.6 75.6	ω ω 4 4	387
ga	S04237	N	507	75.6	34	0
ga	T11559	N	507	75.6	34	C5
gag	FOLJG5	ب	506	75.6	3 4	4
gag	FOLJG3	μ.	506	75.6	34	ω
conserved hypothet	D87363	N	499	75.6	34	N
T16N11.7 protein	E86289	N	399	75.6	34	_
anthranilate phosp	ЈН0099	_	340	75.6	34	0

ALIGNMENTS

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RESULT 2
S24475

C;Species: human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C;Accession: S24475; S24488
                                                                                                          A;Molecule type: DNA A;Residues: 1-75 <SALV.
A;Residues: 1-75 <SALV.
A;Cross-references: EMBL:Z11142; NID:g60101; PIDN:CAA77493.1; PID:g60102 C;Superfamily: AIDS-related virus gag polyprotein C;Keywords: polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-75 <SAL;
A;Cross-references: EMBL:Zl1148; NID:g60078; PIDN:CAA77499.1;
C;Superfamily: AIDS-related virus gag polyprotein
C;Keywords: polyprotein
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gag polyprotein - human immunodeficiency virus type 1 (isolate LV)
N;Alternate names; assemblin; core polyprotein; gag precursor
N;Contains: capsid antigen core protein p24CA; core protein p1; core protein p6;
C;Specles: human immunodeficiency virus type 1, HIV-1
C;Date: 17-May-1985 *sequence_revision 17-May-1985 *text_change 05-Dec-1998
C;Accession: A03948
R;Muesling, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon
Nature 313, 450-458, 1985
N;Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy
A;Reference number: A93355; MUID:85111157; PMID:2982104
A;Accession: A03948
A;Molecule type: DNA
A;Residues: 1-478 <MUE>
C;Genetics:
C;Genetics:
C;Genetics:
C;Superfamily: AIDS-related virus gag polyprotein
C;Keywords: AIDS; blocked amino end; core protein; immunodeficiency; lipoprotein
F;2-4/8/Product: matrix antigen core protein p17MA *status predicted <P17>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polyprotein - human immunodeficiency virus type 1
C;Species; human immunodeficiency virus type 1, HIV-1
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 2
C;Accession: S24476; S24489
R;Salminen, M.
submitted to the EMBL Data Library, October 1991
A;Reference number: S24471
A;Reference number: S24471
A;Accession: S24476
A;Status: preliminary
A;Molecule type: DNA
A;Residues; 1-76 <SALD
A;Cross-references: EMBL:Z11143; NID:g60103; PIDN:CAA77494.1; PID
C;Superfamily: AIDS-related virus gag polyprotein
C;Keywords: polyprotein
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C.Species: human immunodeficiency virus type 1, HIV-1
C.Date: 20-Feb-195 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C.Accession: $24474; $24487
R.Salminen, M.
submitted to the EMBL Data Library, October 1991
A.Reference number: $24471
A.Recession: $24471
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Superfamily: AIDS-related virus gag polyprotein;
Keywords: AIDS; blocked amino end; core protein; immunodeficiency; lipoprotein;
;2-478/Product: gag precursor (assemblin) #status predicted <GAG>
;2-132/Product: matrix antigen core protein p17MA #status predicted <P17>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88.9%;
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Match

Score 40;

DB 2;

Length 498;

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A;Gene: gag
C;Superfamily: AIDS-related virus gag polyprotein
C;Superfamily: AIDS-related virus gag polyprotein
C;Keywords: AIDS; core protein; immunodeficiency; polyprotein
F;1-129/Product: core protein p17 *status predicted <C17>
F;130-389/Product: core protein p24 *status predicted <C24>
F;390-497/Product: core protein p15 *status predicted <C15>
                                                                                                                                                                                                             gag polyprotein - human immunodeficiency virus type 1 (strain JRFL) C;Species: human immunodeficiency virus type 1, HIV-1 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 24-C;Accession: T09436
R;Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; K submitted to the EMBL Data Library, July 1996
                                                                                                                                                                                                                                                                                                                                                            RESULT
T09436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Spire, B.; Sire, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Gene B1, 275-284, 199
Gene B1, 275-284, 199
A;Title: Nucleotide sequence of HIV1-NDK: a highly cytopathic strain of the hu
A;Reference number: JQ0065; MUID:90034200; PMID:2806917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A:Note: host Homo sapiens (man)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C:Accession: JQ0065
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F;110-114/Region: nuclear location signal
F;110-114/Region: nuclear location signal
F;133-363/Product: capsid antigen core protein p24CA #status predicted
F;364-377/Product: core protein p2 #status predicted <CP2>
F;378-432/Product: nucleocapsid core protein p7NC #status predicted <CP
A;Gene: gag
C;Superfamily:
                                             A; Cross-references:
C; Genetics:
                                                                                               A; Molecule type: DNA
A; Residues: 1-498 <P
                                                                                                                                                                  A; Reference number: Z16673
A; Accession: T09436
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                                                                                                                                         A; Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1-497
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F;413-426/Region: zinc finger CCHC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:M27323; NID:g328154; PIDN:AAA44868.1; PID:g32815;
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9; Conserv
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9; Conservative
  AIDS-related virus
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                                                                        EMBL: U63632;
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100.0%; Pr
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                                                                      NID:g1465777; PID:g1465778
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gag
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Pred. No.
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polyprotein
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3.4;
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ed <C17>
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R;Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.
J. Virol. 66, 6587-6600, 1992
A;Title: Complete nucleotide sequence, genome organization, and biological properties of A;Accession: A44001
A;Accession: A44001
A;Mccession: A44001
A;Mc
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A;Title: Nucleotide sequence of the AIDS virus, LAV.
A;Reference number: A90866; MUID:85099333; PMID:2981635
A;Accession: A03946
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F;413-426/Region: zinc finger CCHC motif
F;433-448/Product: core protein pl #status predicted <CPl>
F;439-500/Product: core protein p6 #status predicted <CP6>
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;392,395,400,405/Binding site: zinc (Cys, Cys, His, Cys) #status experimental
F;413,416,421,426/Binding site: zinc (Cys, Cys, His, Cys) #status experimental
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C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change C;Accession: A03946
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F;113-363/product: capsid antigen core protein p24CA #status predicted <P24>
F;133-363/Product: core protein p2 #status predicted <CP2>
F;364-377/Product: nucleocapsid core protein p7NC #status predicted <CP7>
F;378-432/Product: nucleocapsid core protein p7NC
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A; Residues: 1-500 <WAI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 KARVLAEAM 10
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Pred. No.
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predicted <GAG>
    #status predicted <P17>
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C;Superfamily: AIDS-related virus gag polyprotein C;Keywords: core protein; polyprotein F;1-132/product: core protein p17 *status predicted <P17> F;133-391/product: core protein p24 *status predicted <P24> F;392-500/product: core protein p15 *status predicted <P15>
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C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 16-Jul-1999
C;Accession: A25523
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F;133-391/Product: core protein p24 *status predicted <P24>
F;392-500/Product: core protein p15 *status predicted <P15>
                                                                                                                                                                    A;Cross-references: EMBL:211530; NID:g60192; PIDN:CAA77621.1; C;Superfamily: AIDS-related virus gag polyprotein
                                                                                                                                                                                                                                                                           R;Carlini, F.
submitted to the EMBL Data
A;Reference number: S33979
A;Accession: S33979
                                                                                                                                                                                                                                                                                                                                                                 gag polyprotein - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 26-Aug-1999
C;Accession: S33979
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A; Residues: 1-500 <DES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Molecular cloning and primary nucleotide sequence analysis of a distinct hu-A;Reference number: A94136; MUID:87041461; PMID:3490666
A;Accession: A25523
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Proc. Natl. Acad. Sci. U.S.A. 83, 8380-8384, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gag polyprotein - human immunodeficiency virus type 1 (isolate CDC-451)
N; Alternate names: core polyprotein
                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-500 <CAR>
                                                                                                                                                                                                                                                         A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:M13136; NID:g326459; PIDN:AAA44306.1; PID:g326462
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KARVLAEAM
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9; Conser
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9; Conserv
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100.0%;
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                                                                                                       88.9%; Score 40; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                      Library, November 1991
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A;Gene: gag
C;Superfamily: AIDS-related virus gag polyprotein
C;Superfamily: AIDS; core protein; immunodeficiency; po
C;Keywords: AIDS; core protein p17 #status predicted
F;1-134/Product: core protein p24 #status predicte
                                                                                                                                                                                                                                                                      RESULT 14
T01667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N;Alternate names: core polyprotein
N;Contains: core protein p15; core protein p17; core protein p24
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C;Accession: A03947
R;Sanchez-Pescador; R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown-SH Science 227, 484-492, 1985
A;Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).
A;Reference number: A04003; MUID:85090453; PMID:2578227
A;Accession: A03947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, July 1989
A; Reference number; S54377
A; Accession: S54377
A; Status: preliminary
A; Molecule type: genomic RNA
A; Residues: 1-501 <THE>
A; Residues: 1-501 <THE>
A; Cross-references: EMBL:M22639; NID:g329377; PIDN:AAA45365.1; PID:g329380
C; Superfamily: AIDS-related virus gag polyprotein
C; Keywords: polyprotein
                                                                R;Allzon, M.; Wain-Hobson, S.; Gluckman, J.C.; Sonigo, P. Cell 46, 63-74, 1986
A;Title: Genetic variability of the AIDS virus: Nucleotide A;Reference number: Z14389; MUID:86245056; PMID:2424612
A;Accession: T01667
                                                                                                                                                                          gag polyprotein - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #t.
C;Accession: T01667
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
"atches 9; Conserv
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(;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 26-Aug-1999
C;Accession: S54377
R;Theodore, T; Buckler-White, A.J.
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                       A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;135-393/Product: F;394-502/Product:
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A; Residues: 1-502 <SAN>
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      A; Residues:
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type: mRNA:
1-505 <ALI
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9; Conservative
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protein p15 #status
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Pred. No.
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19-Feb-1999 #text_change
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3.4;
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Search completed: March Job time: 9.81818 secs

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gag polyprotein - human immunodeficiency virus type 1 (strain MN)
N;Alternate names: core polyprotein
N;Contains: core protein pl; core protein pl7; core protein p2; core protein p24;
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 26-Feb-1999
C;Accession: A38068
R;Henderson; L.E.; Bowers, M.A.; Sowder II, R.C.; Serabyn, S.A.; Johnson, D.G.; Be
J; Virol. 66, 1856-1865, 1992
A;Title: Gag proteins of the highly replicative MN strain of human immunodeficienc A;Accession: A38068; MUID:92194415; PMID:1548743
A;Accession: A38068; MUID:92194415; PMID:1548743
A;Residues: 1-506 (HEN)
C;Genetics:
                                                                                                                                                             A;Gene: 9ag
A;Gene: 9ag
A;Gene: 9ag
A;Gene: 9ag
A;Gene: 9ag
C;Superfamily: AIDS-related virus gag polyprotein
C;Keywords: AIDS; core protein; immunodeficiency; polyprotein
F;1-134/Product: core protein p17 *status experimental <P17>
F;135-365/Product: core protein p24 *status experimental <P24>
F;366-379/Product: core protein p2 *status experimental <PP2>
F;380-434/Product: core protein p7 *status experimental <PP7>
F;435-450/Product: core protein p1 *status experimental <PP1>
F;451-506/Product: core protein p6 *status experimental <PP6>
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                                                                                                      Query Match
Best Local
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361 KARVLAEAM
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                                                                                                      Local Similarity
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                      2 KARVLAEAM 10
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9; Conser
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369
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100.0%; Pr
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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B97591
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A;Reference number: S72584
A;Accession: S72820
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ALIGNMENTS

cosmid B1620

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A; Cross-references: C; Genetics:
                                                                                                                                                                                                 C;Accession: S72978
R;Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993
A;Description: Mycobacterium leprae cosmid B229.
A;Reference number: S72588
A;Accession: S72978
                                                                                                                                                                                                                                                                                      hypothetical protein B229_C1_175 - Mycobacterium leprae C;Species: Mycobacterium leprae C;Date: 19-Mar_1997 #sequence_revision 25-Apr-1997 #text_change
 밁
                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-263 <SMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-122 <SMI>
                                                                                                                A; Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:U00015; NID:g466931; PIDN:AAC43229.1; PID:g466941
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Matches 8
                                                     Query Match
Best Local Similarity
Matches 8; Conserv
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218 ERARVVAEAA 227
                            1 EKARVLAEAA 10
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8; Conser
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80.0%;
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Pred. No. 4.8;
2; Mismatches
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A.; Liu, F.; Wollam, C.; Allinger, M.; Science 294, 2323-2328, 2001
A;Title: Genome Security
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: H70725
R;Cole, S.T.; Brosch, R,; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, R; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares,
                                                                                                                                                                                   RESULT
B97591
                                                                                            C;Date: 30-Sep-2001 *sequence_revision 30-Sep-2001 *text_change 11-Jan-2002 C;Accession: B97591
                                                                                                                                      50S ribosomal protein L17 nma0102 [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                             S
                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:Z77724; GB:AL123456;
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv2585c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R:Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; leam, M.A.; Rutherford, K.M.; Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, I.A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, I.A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, I.A;Artile: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: G86956
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A; Residues: 1-557 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A:Reference number: A70500; MUID:98295987; PMID:9634230 A;Accession: H70725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rajandream, M.A.; Rogers,
Nature 393, 537-544, 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: G86556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; nucleic acid sequence not shown; translation not
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218 ERARVVAEAA 227
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      Plant Pathogen
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Pred. No.
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Pred. No. 5
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                                               Miller, N.; F
Doughty, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NID:g3261620; PIDN:CAB01258.1; PID:e256146;
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    Biotechnology
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                                                                     Blanchard,
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                                            Scott,
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                                            M.; Qurollo, B.; Gold
; Lappas, C.; Markelz,
    Agent Agrobacterium
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kelz, B.;
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Holroyd,
                                                                                                                                                           C58,
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G81895
                        A; Experimental source: C; Genetics:
                                                                   A; Molecule type: DNA
A; Residues: 1-298 <PAR>
A; Cross-references: GB:AL162755;
                                                                                                                                                    A;Title: Complete DNA sequence of a serogroup A strain of A;Reference number: A81775; MUID:20222556; PMID:10761919 A;Accession: G81895
                                                                                                                                                                                                                     R; Parkhill, J.; Achtman, M.; James, ; Holroyd, S.; Jagels, K.; Leather, Nature 404, 502-506, 2000
                                                                                                                                                                                                                                                                                      probable acetylglutamate kinase (EC 2.7.2.8) NMA1275 [imported] - Neisseria C;Speckes: Neisseria meningitidis C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001 C;Accession: G81895
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                                                                                                                                A; Status: preliminary
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argB;

NMA1275

serogroup

GB:AL157959; NID:g7379742; A, strain 22491

PIDN:CAB84528.1; PID:g737

K.D.; Bentley,
S.; Moule, S.;

S.D.; Churcher, C.; Mungall, K.; Quail,

Klee, M.A.;

S.R.; Mo Rajandre

meningiti

Neisseria menigitidis 22491

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C;Accession: AH2812
R;Accession: AH2812
R;Accession: Setubal, J.C.; Kaul, R.; Monks, erage, G.; Gillet, W.; Grant, C.; Guenthner, E; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
                                                                                                                                            A; Map position: circular chromosome C; Superfamily: Escherichia coli ribosomal protein
                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-141 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL42918.1; PID:g17740374; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                     ster, E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium A;Reference number: AB2577; PMID:11743193

A;Accession: AH2812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50S ribosomal protein L17 [imported] - Agrobacterium tumefaciens (strain C5 C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Map position: circular ch
C; Superfamily: Escherichia
                                                                                                                                                                                      A; Gene:
                                                                                                                                                                                                                                                                                                   A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-141 <KUR>
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A;Accession: B97591
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Pred. No. 6.5;
1; Mismatches
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                                                                                                         Score 36;
                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              P.; Jung, M.;
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D.; Kutyavin, T.; Levy, R.; Li, M.; McCl
                                                                                                         <sub>د</sub>
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acetylglutamate kinase NMB1074 [imported] - Neisseria meningitidis (strain MC58 serogrou C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: E81124
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J., Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: E81124
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-298 <TET>
A;Residues: 1-298 <TETE>
A;Gene: NMB1074
C;Superfamily: acetylglutamate kinase
C;Senerics: Serogroup B, strain MC58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   " Query Match
Best Local S
                                                                                                                                                                                                               gag polyprotein - human immunodeficiency virus type 1 (fragment)
N:Contains: p24 protein; p25 protein; p7 protein
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 26-Jul-1996 #text_change 26-Aug-1999
C:Accession: S24478; S24484
R:Salminen, M.
submitted to the EMBL Data Library, October 1991
A:Reference number: S24471
A:Recession: S24478
A:Recession: S24478
A:Recession: S24478
A:Recession: S24471
A:Accession: S24478
A:Residues: 1-75 <SAL>
A:Cross-references: EMBL:Z11148; NID:g60078; PIDN:CAA77499.1; PID:g939876
C:Superfamily: AIDS-related virus gag polyprotein
C:Keywords: polyprotein
RESULT 10
S24475
gag polyprotein -
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C; Keywords: phosphotransferase
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                                2 KARVLAEA 9
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gag polyprotein - human immunodeficiency virus type 1 C;Species: human immunodeficiency virus type 1, HIV-1 C;Date: 20-Feb-1995 *sequence_revision 20-Feb-1995 *tec C;Accession: S24474; S24487
R;Salminen, M.
submitted to the EMBL Data Library, October 1991
A;Reference number: S24471
A;Accession: S24474
A;Status: preliminary
A;Status: preliminary
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C;Date: 20-Feb-1995 *sequence_revision 20-Feb-1995 *text_change 26-Aug-1999
c;Accession: S24475; S24488
R;Salminen, M.
submitted to the EMBL Data Library, October 1991
A;Reference number: S24471
                                                                    A;Cross-references: EMBL:211143; NID:g60103; PIDN:CAA77494.1; PID:g60104 C;Superfamily: AIDS-related virus gag polyprotein C;Keywords: polyprotein
                                                                                                                                                                                                                                                    gag polyprotein - human immunodeficiency virus type 1 C;Species: human immunodeficiency virus type 1, HIV-1 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #tC;Accession: S24476; S24489
                                                                                                                                                                                                 submitted to the EMBL Data Library, October 1991 A; Reference number: $22471
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A; Residues: 1-75 < SAL>
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A; Residues: 1-75 <SAL>
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A; Residues: 1-76 <SAL>
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A; Residues: 1-423 <KAW>
A; Cross-references: DDBJ:AP000063; NID:g5105654; PIDN:BAA81210.1; PID:g5105898
A; Experimental source: strain K1
C; Genetics:
A; Gene: APE2199
C; Superfamily - ----
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C; Superfamily: AIDS-related virus gag polyprotein
C; Superfamily: AIDS; blocked amino end; core protein; immunodeficiency; lipoprotein;
F; 2-478/Product: gag precursor (assemblin) #status predicted <GAG>
F; 2-132/Product: matrix antigen core protein p17MA #status predicted <P17>
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                                                                                                                                                                                                           F;392-405/Region: zinc finger CCHC motif
F;413-426/Region: zinc finger CCHC motif
F;247-405/Region: zinc finger CCHC motif
F;27/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;392,395,400,405/Binding site: zinc (Cys, Cys, His, Cys) #status experimental
F;413,416,421,426/Binding site: zinc (Cys, Cys, His, Cys) #status experimental
                                                                                                                                                                                                                                                                                                                                                         F:20-32/Region: nuclear location signal
F:110-114/Region: nuclear location signal
F:133-363/Product: capsid antigen core protein p24CA #status predicted <P24>
F:364-377/Product: core protein p2 #status predicted <CP2>
F:378-432/Product: nucleocapsid core protein p7NC #status predicted <CP7>
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A;Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrov. A;Reference number: A93355; MUID:85111157; PMID:2982104
A;Accession: A03948
A;Molecule type: DNA
A;Residues: 1-478 <MUE>
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W;Alternate names: assemblin; core polyprotein; gag precursor

N;Contains: capsid antigen core protein p24CA; core protein p1; core protein
C;Specles: human immunodeficiency virus type 1, HIV-1
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 05-Dec-1998
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C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Aug-1999 *sequence_revision 20-Aug-1999 *text_change 20-Jun-2000
C;Accession: B72528
R;Kawarzabayasi Y; Hino, Y; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.;
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki,
DNA Res. 6, 83-101, 1999
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  359 KARVLAEA 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.5%;
                                                                                                                                                                     79.5%;
                                                                                                             s; Score 35; DB; Pred, No. 34; O; Mismatches
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C:Superfamily: AIDS-related virus gag polyprotein C:Keywords: AIDS; core protein; immunodeficiency; poly F:1-129/Product: core protein p17 *status predicted CF:130-389/Product: core protein p24 *status predicted F:390-497/Product: core protein p15 *status p15 *sta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gag polyprotein - human immunodeficiency virus type 1 (isolate NDK)

N;Alternate names: core polyprotein
N;Contains: core protein pl5; core protein pl7; core protein p24
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C;Accession: J00065
R;Spire, B; Sire, J; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.
Gene 81, 275-284, 1989
Search completed: March Job time: 11.8182 secs
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A;Accession: JQ0065
A;Molecule type: DNA
A;Residues: 1-497 <SPI>
A;Residues: 1-497 <SPI
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       protein search, using
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O9hgz8 pyrococus
O8be41 agrobacter1
O92na6 rhizobium m
O9j122 human immun
O9j141 human immun
O9j140 human immun
O9j144 human immun
O9j144 human immun
O9j148 human immun
O9j198 human immun
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Q96k21 homo sapien
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Q49858 mycobacteri
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ALIGNMENTS

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MEDLINE-21396507; PubMed-11481430;
Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.
Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.
Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
**Analysis of the chromosome sequence of the legume symbiont
**Sinorhizobium meliloti strain 1021.**, **Analysis of the chromosome sequence of the symbiont
**Sinorhizobium meliloti strain 1021.**, **Analysis of the chromosome sequence of the legume symbiont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O92LE1 PRELIMINARY; PRT; 152 AA.

O92LE1;
O1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Putative transposase number 1 for insertion sequence ISRM28.
TRM28.1 OR RO3124 OR SMC03278.
Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                            Sinorhizobium meliloti strain 1021.";
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
EMBL; AL591793; CAC47703.1;
InterPro; IPR002514; Transposase_8.
Pfam; PF01527; Transposase_8; 1.
                                                                                                                                                                      Complete proteome. SEQUENCE 152 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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  41
                                          1 EKARVLAEAA 10
FITT : FITT
                                                                                  Similarity 80.88; Conservative
  50
                                                                                                                                                                        16544 MW;
                                                                                                      90.9%;
                                                                                                      Score 40;
Pred. No.
                                                                                                                                                                        F518578357FF0C5C CRC64;
                                                                                      Mismatches
                                                                                                      DB 16; Length 152;
                                                                                      Indels
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Best Local S
Matches 8
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Best Local S
Matches 8
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Submitted (MAR-1994) to the E
-!- SIMILARITY: STRONG, TO M.
EMBL; U00015; AAC43229.1; -.
Hypothetical protein; Signal.
SIGNAL 1 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q49858 PRELIMINARY; PKI, 2000, 2049858; Q49858; Q49858; Q1-808-1996 (TrEMBLrel. 01, Created) Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update) Q1-NEB-1997 (TrEMBLrel. 02, Last annotation update) Q1-PEB-1997 (TrEMBLrel. 02, Last annotation update) Hypothetical 27.4 kDa protein B229_C1_175 precursor B229_C1_175.
Q9CCV3;
Q9CCV3;
01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     smith D.R., Robison K.; Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases -!- SIMILARITY: STRONG, TO M.TUBERCULOSIS MTCY78.14. EMBL; U00020; AAA17292.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein; Signal. SIGNAL 1 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium leprae.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bactinomycetales; Corynebacterineae; Mycobacteriaceae; M
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01-FEB-1997 (TrEMBLrel.
Hypothetical 12.9 kDa pr
B1620_C3_232.
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01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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                                                                                                                                                                                                          218
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8; Conserv
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8; Conser
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122 AA;
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ilarity 80.0%;
Conservative
(TrEMBLrel.
                                                                              PRELIMINARY;
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BLrel. 02, Last annotation update)
kDa protein B1620_C3_232 precursor.
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                                                                                                                                                                                                                                                                                                                                              86.4%;
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Created)
Last sequence update)
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Pred. No. 6.8;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                2;
                                                                                                                                                                                                                                                                                                                                      Score 38;
Pred. No.
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HYPOTHETICAL
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                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                 POTHETICAL PROTEIN B229_C1_175
7BBA3900F8911DF4 CRC64;
                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                281
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CRC64;
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RESULT
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Best Local
                        Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBan)
EMBL; RK027746; BAB55338.1; -
EMBL; BC015738; AAH15738.1; -
InterPro; IPR000564; 2Fe2S_ferredoxin.
InterPro; IPR000345; CytC_heme_bind.
InterPro; IPR000306; Znf_FYVE.
Pfam; PF01363; FYVE; 1
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Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suz
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
Wagatsuma M., Chiba Y., Ishida S., Murakawa K., Ono Y., Ta
Watanabe S., Kimura K., Murakami K., Ishil S., Kawal Y.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masul
Ninomiya K., Iwayanagi T.;
*NEDO human cDNA sequencing project.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
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Q96K21;
Q1-DEC-2001
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MEDLINE-1128732; PubMed-11234002;
Cole S.T., Eiglmeter K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Wingall K., Basham D., Brown D., Chillingworth T., Connor R.,
Mungall K., Basham D., Brown D., Chillingworth T., Fraser A., Hamlin N.
Holroyd S., Hornsby T., Jagels K., Lacrolx C., Maclean J., Moule S.,
Holroyd S., Hornsby T., Jagels K., Lacrolx C., Maclean J., Moule S.,
Murphy L., Oliver K., Ouall M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Squares S., Stevens K., Taylor K., Whitchead S., Woodward J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein).

Homo sapiens (Human).

Homo sapiens (Human).

Tharvota; Metazoa; Chordata; (hordata; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 20, Last annotation update)
CDNA FLJ14840 fis, clone OVARC1001916 (Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein; Complete SEQUENCE 281 AA; 29333 MW;
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Bacteria; Firmicutes; Actinobacteria;
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                                                                                                                                                                                                                                                                                                     TISSUE=RETINA;
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-9606;
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8; Conserv
PS00197;
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2FE2S_FERREDOXIN; UNKNOWN_1.
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Pred. No.
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Murakawa K., Ono Y., Takiguchi S.,
. Ishil S., Kawal Y., Saito K.,
a Y., Nagahari K., Masuho Y.,
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
50s ribosomal protein L17.
RPLQ OR ATU1922 OR AGR_C_3516.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES-P.furiosus; STRAIN-VC1 / DSM 3638 / ATCC 43587 / JC Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.; "The complete sequence of the Pyrococcus furiosus genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-JUN-2002 (TrEMBLrel. 21, Hypothetical protein PF1746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9HGZ8;
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SEQUENCE FROM N.A. MEDLINE-21608550;
                                                                                                        Agrobacterium tumefaciens (strain C58 / ATCC Bacteria; Proteobacteria; alpha subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mol. Microbiol. 38:684-693(2000).
EMBL; AE010273; AAL81870.1; -.
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Horlacher R., Robb F.T., Boos W., Weiss
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                                                              Rhizobiaceae; Rhizobium.
NCBI_TaxID=176299;
                                                                                                                                                                                                                                                                                           Q8UE41
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"Evidence of recent lateral gene transfer among
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (FEB-2002)
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AF307052; AAG45379.1;
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637 AA; 72701 MW; EBFA42F42FB5A428 CRC64;
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  PubMed=11743193;
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Pred. No. 58;
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Rhizobiaceae
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Q92NA6;
Q92NA6;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein R02307.
R02307 OR SMC01556.
Rhizoblum meliloti (Sinorhizoblum meliloti).
Rhizoblum meliloti (Sinorhizoblum subdivision; Rhizoblaceae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S.;
"Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58.";
Science 294:3233-2338(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L. Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Katyavin C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordo Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry Gordon Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                      Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut Boistard P., Becker A., Boutry M., Cadleu E., Dreano S., Gloux S. Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.; "Analysis of the chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021.", Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
                                                            Hypothetical
SEQUENCE 2
                                                                                                                                                                                                                                              STRAIN-1021
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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   Conservative
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986D78DE6DDE79F2 CRC64;
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01-MAR-2002;
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01-OCT-2000
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EMBL; AF219292; AAF30198.1; -.
HSSP; P05888; 1AAF.
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Leinikki P., Salminen M.O.;
"Analysis of HIV-1 genetic subtypes in Finland reveals good
correlation between molecular and epidemiological data.";
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Leinikki P., Salminen M.O.;
"Analysis of HIV-1 genetic subtypes in
correlation between molecular and epide
Scand. J. Infect. Dis. 0:0-0(2000).
EMBL; AF219351; AAF30257.1; *.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; Retroid viruses; NCBI_TaxID=11676;
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                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                           SMART; SM00343; ZnF_C2HC; 1.
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Viruses; Retroid viruses; Retroviridae;
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hes 8; Conserv
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8; Conserv
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Pred. No.
                                                                                                                                                 Score 35;
Pred. No.
                                                                                                                                                                                                                                     94C21F799195F4AC CRC64;
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                                                                                                                                                 DB 15;
12;
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RESULT
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SEQUENCE
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Q9J140;
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Leinikki P., Salminen M.O.;
"Analysis of HIV-1 genetic subtypes in Finland rev
correlation between molecular and epidemiological
Scand. J. Infect. Dis. 0:0-0(2000).
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EMBL; AF219356; AAF30262.1;
HSSP; P05888; 1AAF.
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Leinikki P., Salminen M.O.;
"Analysis of HIV-1 genetic subtypes in Finland reveals good
correlation between molecular and epidemiological data.";
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Pfam; PF00098; zf-CCHC; 1.
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Viruses; Retroid viruses; Retroviridae;
                                                                                                                                                        SMART; SM00343; ZnF_C2HC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus type 1.
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8; Conserv
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8; Conserv
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Last sequence update)
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                          Score 35;
Pred. No.
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Pred. No.
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Leinikki P., Salminen M.O.;
"Analysis of HIV-1 genetic subtypes in
correlation between molecular and epide
Scand. J. Infect. Dis. 0:0-0(2000).
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Leinikki P., Salminen M.O.;
"Analysis of HIV-1 genetic subtypes in Finland reveals good
correlation between molecular and epidemiological data.";
Scand. J. Infect. Dis. 0:0-0(2000).
EMBL; AF219229; AAF30235.1; -.
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SMART; SM00343; znf_C2HC; 1.
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Leinikki P., Salminen M.O.;
"Analysis of HIV-1 genetic subtypes in Fi
correlation between molecular and epidem1
Scand. J. Infect. Dis. 0:0-0(2000).
EMBL; AF219275; AAF30181.1; -.
HSSP; PD5888; IAAF.
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Viruses; Retroid viruses; Retroviridae;
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EMBL; AE007100; AAK46975.
TIGR; MT2662; -
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 InterPro; IPR000914; SBP_bac_5
                    Rv2585c;
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MEDLINE-9295987; pubMed-9634230;
GCOLE S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris GCOLE S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
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01-NOV-1997 (Rel. 35, Created)

01-NOV-1997 (Rel. 35, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

Hypothetical lipoprotein Rv2585c precursor.

RV2585C OR MT2662 OR MTCY227.16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
-!- SUBCELLULAR LOCATION: Attached to the membrane by a
(Probable).
-!- SIMILARITY: STRONG, TO M.LEPRAE ML0489 AND DCIAE.
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
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Corynebacterineae; Mycobacteriaceae; Mycobacterium
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Interpro: IPR004662; Aaglukinase.
Interpro: IPR001657; Glu_5kinase.
Pfam; PF00696; aakinase; 1.
PRINTS; PR00474; GLU5KINASE.
TIGRAD9761; args; 1.
Arginine biosynthesis; Transferase; Kinase; Compsequence 298 AA; 31269 MW; 7A027E52D5BAIA74
                                                                                                                                                                                                                                                                                                 Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd Jagels K., Leather S., Moule S., Mungall K., Quall M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.; "Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491.";
Nature 404.502-506(2000).
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                                                                                                                                                                 the European Bloinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fc entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-Z2491 / Serogroup A / Serotype 4A; MEDLINE-20222556; PubMed-10761919;
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Bacteria; Proteobacteria; beta suk
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ARGB OR NMA1275.
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Acetylglutamate kinase (EC 2.7.2.8) (NAG kinase) (AGK) (N-acetyl-L-
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15-JUN-2002
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glutamate 5-phosphate.

PATHWAY: Arginine blosynthesis; second step.

SUBCELLULAR LOCATION: Cytoplasmic (Potential).

SIMILARITY: BELONGS TO THE ACETYLGLUTAMATE KINASE FAMILY.
                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through
sen the Swiss Institute of Bioinformatics and the EN
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HYPOTHETICAL LIPOPROTEIN RV2585C.
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                                NO ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.6;
                                                                                                                                                                                              ormatics and the EMBL outst There are no restrictions on as its content is in
                                5, DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A
                                         1;
                                                                         Complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                       0
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                                        Length 298
                                                               CRC64;
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                                                                                                                                                                                                                                                                                         N-acetyl-L-
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                      Gaps
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 RESULT 4
GAG_HV1W2
ID GAG_H
AC P0588
DT 01-N0
DT 01-FE
DT 16-OC
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                                                                                                                                    Query Match
Best Local S
Matches 7
GAG_HV1W2
P05889;
01-NOV-1988
01-FEB-1994
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glutamate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARGB_NEIMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=491;
                                                                                             11
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                                                                                                         1 EKARVLAEA
                                                                                              DKARILAEA
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 (Rel.
(Rel.
(Rel.
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SEQUENCE FROM N.A.

SETRAIN=MC58 / Serogroup B;

MEDLINE=2017575; pubMed=10710307;

MEDLINE=20175755; pubMed=10710307;

Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,

Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,

Melson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,

Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,

Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B.,

Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,

Gill J., Scarlato V., Masignani V., Pilza M., Grandi G., Sun L.,

Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;

"Complete genome sequence of Neisseria meningitidis serogroup B strain

MC58.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGREAMS; TIGR00761; argB; 1.
Arginine biosynthesis; Transferase; Kinase; Complete proteome SEQUENCE 298 AA; 31283 MW; 7A19DFE8D5BA1A74 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- CATALYTIC ACTIVITY: ATP + N-acetyl-L-glutamate = ADP + N-glutamate 5-phosphate.
-i- PATHMAY: Arginine blosynthesis; second step.
-i- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-i- SIMILARITY: BELONGS TO THE ACETYLGLUTAMATE KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Acetylglutamate kinase (EC 2.7.2.8) (NAG kina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001048; Aa_kinase.
InterPro; IPR004662; AcgluKinase.
InterPro; IPR001057; Glu_5kinase.
Pfam; PF00696; aakinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE002458; AAF41469.1; -. TIGR; NMB1074; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 287:1809-1815(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria meningitidis (serogroup
Bacteria; Proteobacteria; beta sul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glutamate 5-phosphotransferase).
aRGB OR NMB1074.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00474; GLU5KINASE.
TIGRFAMs; TIGR00761; argB; 1
                                                                                                                                                                                                                                                                                                                                            Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                           9
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09, Created)
28, Last sequ
40, Last anno
                                                                                                                                                                                                                                                                                                                                                                        81.8%;
77.8%;
sequence up annotation
                                                                                                                                                                                                                                                                                                                                            2;
                                                                                                                                                                                                                                                                                                                                                                     Score
Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
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                           update)
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6.3;
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                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                             Length 298;
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update)

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GAG_HYDE

GAG_HYDE

ID GAG_H

ID GAG_H

AC P2473

AC P2473

AC P2473

DT 01-M2

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DE GAG F

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GN GAG F

GN GAG F

OS (HITVE

OC Virus
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Best Local S
Matches
                                                                                                                     GAG_HV1U4
P24736;
                                                                         01-MAR-1992 (Rel.
01-FEB-1994 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-86235450; PubMed-3012778; Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D., Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.; "Genetic variation in HTLV-III/LAV over time in patients with AIDS at risk for AIDS."; Science 232:1548-1553(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000721; Gag_p24.
InterPro; IPR000071; Retrovir_p17.
Pfam; PF00540; Gag_p17; 1.
Pfam; PF00607; Gag_p24; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                      NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P03351; 1EIA.
HIV; K03457; GAG$WMJ2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; K03457; AAB12988.1; -. HSSP; P03351; 1EIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAG polyprotein [Contains: Core proteins P17, P24, (Fragment).
                            Human immunodeficiency virus type 1 (strain Ugandan
                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus
               (HIV-1).
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                                                                                                                                                                                                                358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE ASSEMBLY, BUDDING, MATURATION, AND INFECTION STACES OF THE VIRAL REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL. GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.

PTM: THE P24 PROTEIN IS PHOSPHORYLATED.

MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTM: THE P24 PROTEIN IS PHOSPHORYLATED.
MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBT
BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD
WAS PERINATALLY INFECTED BY HER MOTHER.
                                                          polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                KARVLAEA 365
                                                                                                                                                                                                                                             KARVLAEA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Core protein;
                                                                                                                                                                                                                                                                           Similarity
8; Conser
Retroid viruses; Retroviridae; Lentivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Retroid
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1
132
363
377
                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                     STANDARD;
                                                         1. 21, Created)
1. 28, Last sequence update)
1. 41, Last annotation update)
[Contains: Core proteins P17,
                                                                                                                                                                                                                                                                                                                                                                               0
131
362
376
>388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polyprotein; Myristate; Phosphorylation
                                                                                                                                                                                                                                                                                                                                       43314
                                                                                                                                                                                                                                                                                       79.5%;
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Retroviridae; Lentivirus
                                                                                                                                                                                                                                                                                                                                      WW;
                                                                                                                                                                                                                                                                                       Score 35;
Pred. No.
                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.

CORE PROTEIN P17 (MATRIX PROTEIN).

CORE PROTEIN P24 (CORE ANTIGEN).

CORE PROTEIN P2.

CORE PROTEIN P7 (NUCLEOCAPSID PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                    MYRISTATE
                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                      EF885BE10ECF7804 CRC64;
                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                     492
                                                                                                                                                                                                                                                                                       DB 1;
13;
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                                                                                                                                     A
                                                          P24,
                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                       Length 388;
                                                          Ρ2,
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                               isolate U455)
                                                          P7,
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                                                            Ρ1,
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                                                                                                             RESULT 6
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Best Local
                                                                                                                                                                                          Matches
                       GAG_HVIND STANDAND,
P18800;
P18800;
01-NOV-1990 (Rel. 16, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Core proteins P17,
                                                                                                                                                                                                                                                         CHAIN
CHAIN
CHAIN
CHAIN
CHAIN
CHAIN
CHAIN
ZN_FING
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00098; zf-CCHC; 2.
pfam; PF00540; Gag_D17; 1.
pfam; PF00507; Gag_D24; 1.
pRINTS; PR00939; CZHCZNFINGER.
PRINTS; PR00234; HIVIMATRIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-91090981; PubMed-2265025;
Th. Downing R.G., Roff M., Clegg J.C.S.,
                                                                                                                                                                                                                                                LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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Human immunodeficiency virus type 1 (NDK isolate) (HIV-1). Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                              AIDS; Core protein;
Zinc-finger; Repeat
                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00343; ZnF_C2HC; 2
PROSITE; PS50158; ZF_CCHC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000721; Gag_p24.
InterPro; IPR000071; Retrovir_p17.
InterPro; IPR001878; Znf_CCHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M62320; AAA75018.1; -. HSSP; P05888; 1AAF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=11703;
                                                                                                                                             354 KARVLAEA
                                                                                                                                                                  2 KARVLAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTM: THE P24 PROTEIN IS PHOSPHORYLATED. SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                         Similarity
8; Conserv
                                                                                                                                                                                                                                     492
                                                                                                                                                                                        79.5%;
llarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                               Repeat.
                                                                                                                                                                    9
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                                                                                                                                                                                                                                                          127
358
371
425
441
492
400
                                                                                                                                                                                                                                                                                                                                                                       Polyprotein;
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                                                                                                                                                                                                                                       ₹.
                                                                                                                                                                                                                                  CORE PROTEIN P24 (CORE ANTI-
CORE PROTEIN P2.

CORE PROTEIN P7 (NUCLEOCAPS
CORE PROTEIN P1.
CORE PROTEIN P6.
CCHC-TYPE 1.
CCHC-TYPE 2.
MYRISTATE (BY SIMILARITY).
M; E4A3B4D633BB6972 CRC64;
                                                                                                                                                                                          0;
                                                                                                                                                                                        Score 35; DB Pred. No. 16, 0; Mismatches
                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY CORE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                         Myristate; Phosphorylation;
                                                                                                                                                                                                   DB
16;
                                                                                                                                                                                                                                                                                                                                         P17
                                                                                                                                                                                                               -:
                                                                                                                                                                                                                                                                                                       (NUCLEOCAPSID PROTEIN).
                                P24, P2, P7,
                                                                                                                                                                                                                                                                                                                            (MATRIX PROTEIN) (CORE ANTIGEN).
                                                                                                                                                                                          0;
                                                                                                                                                                                                               Length 492;
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RESULT 7
GAG_HV10Y
ID GAG_H
AC P2088
DT 01-FE
DT 01-FE
DT 115-JU
                                                                                                                            Query Match
Best Local Similarity
Whiches 8; Conserv
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                                                                                                8
                                                                                                                                                                               GAG_HV1OY STANDARD: PRT; 498 AA. P20889; O1-FEB-1991 (Rel. 17, Created) O1-FEB-1994 (Rel. 28, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                         ZN_FING
ZN_FING
LIPID
                                                                                                                                                                                                                                                                                                                                     Pfam; PF00098; zf-CCHC; 2.
Pfam; PF000540; Gag_p17; 1.
Pfam; PF000507; Gag_p24; 1.
PRINTS; PR00939; C2HCZNFINGER.
PRINTS; PR00934; HIVIMATRIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                              AIDS; Core pa
Zinc-finger;
                                                                                                                                                                                                                                                                                                                  SMART; SM00343; ZnF_C2HC; ; PROSITE; PS50158; ZF_CCHC;
                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000721; Gag_p24.
InterPro; IPR000071; Retrovir_p17.
InterPro; IPR001878; Znf_CCHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M27323; AAA44868.1; -. PIR; JQ0065; FOLJND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=90034200; PubMed=2806917;
Spire B., Sire J., Zachar V., Rey F., Barre-Sinoussi F., Galibert F.,
Hampe A., Chermann J.C.;
                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P05888; 1AAF.
HIV; M27323; GAG$NDK.
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                                                                                                355
                                                                                                                    N
                                                                                               KARVLAEA 362
                                                                                                                  KARVLAEA 9
                                                                                                                                                                                                                                                                                                         protein;
                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                               Repeat.
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359
374
429
445
404
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                                                                                                                                                                               55152
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                                                                                                                                                Score 35;
Pred. No.
                                                                                                                                                                                                  CORE PROTE
CORE PROTE
CCHC-TYPE
CCHC-TYPE
                                                                                                                                                                              MYRISTATE (BY SIMILARITY)
F50A42E42CCF20AA CRC64;
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                                                                                                                                                 DB 1;
16;
                                                                                                                                                                                                                                           (NUCLEOCAPSID PROTEIN).
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                                                                                                                                                                                                                                                               (MATRIX PROTEIN) (CORE ANTIGEN).
                                                                                                                                                        Length 496;
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RESULT 8
GAG_HV1C4
ID GAG_H
AC P0588
DT 01-NC
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Best Local
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GAG_HV1C4 STANDARD;
P05887;
01-NOV-1988 (Rel. 09, Created)
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ZN_FING
LIPID
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InterPro; IPR000071; Retrovir_p17.
InterPro; IPR001878; Znf_CCHC.
Pfam; PF00098; Zf-CCHC; 2.
Pfam; PF00540; Gag_p17; 1.
Pfam; PF00607; Gag_p24; 1.
                                                                                                                                                                                                                                                                                      CHAIN
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Zinc-finger;
                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0939; C2HCZNFINGER. PRINTS; PRO0234; HIVIMATRIX. SMART; SM00343; ZnF_C2HC; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Huet T., Dazza M.C., Brun-Vezinet F., Roelants G.E., Wain-Hobson: "A highly defective HIV-1 strain isolated from a healthy Gabonese individual presenting an atypical western blot.";

AIDS 3:707-715(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus type 1 (OYI isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                             CHAIN
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AIDS; Core protein; Polyprotein; Myristate;
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                                                                                                                                                                                                                                                                                                                                           INIT_MET
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                                                                                                358
                                                                                                               2 KARVLAEA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL. GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.

PTM: THE P24 PROTEIN IS PHOSPHORYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HEALTHY GABONESE INDIVIDUAL.
SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
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CORE PROTEIN P

CORE PROTEIN P

CORE PROTEIN P
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MYRISTATE (BY SIMILARITY).
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                                                                                                                                                                 Score 35;
Pred. No.
                                                                                                                                                                                                        BDFF20658DEB20B1 CRC64;
                                                                                                                                                   Mismatches
                                499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                 16;
                                                                                                                                                                            DB 1;
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P6
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                                                                                                                                                                                                                                                                                                                                                                   Phosphorylation;
                                                                                                                                                                                                                                                                                     (NUCLEOCAPSID PROTEIN)
                                                                                                                                                   0,:
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InterPro; IPR000721; Gag_p24.

InterPro; IPR000711; Retrovir_p17.

InterPro; IPR001878; Znf_CCHC.

Pfam; PF00098; Zf-CCHC; 2.

Pfam; PF00540; Gag_p17; 1.

Pfam; PF00607; Gag_p24; 1.

PRINTS; PR00939; CZHCZNFINGER.

PRINTS; PR00934; HIVIMATRIX.

SMART; SM00343; ZNF_CZHC; 2.

PROSITE; PS50158; ZE_CCHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWI
between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Molecular cloning and primary nucleotide sequence analysis of a distinct human immunodeficiency virus isolate reveal significant divergence in its genomic sequences."; proc. Natl. Acad. Sci. U.S.A. 83:8380-8384(1986).

-1- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL. GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.

-1- PTM: THE P24 PROTEIN IS PHOSPHORYLATED.

-1- SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
                                                                                                                                            ZN_FING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-
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15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                          AIDS; Core protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-87041461; PubMed-3490666;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus type 1 (CDC-451 isolate) (HIV-1). Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAG polyprotein
                                                                                                                SEQUENCE
                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                            Zinc-finger;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Desai S.M., Kalyanaraman V.S., Casey J.M.,
358
                                                                      Local
                            2 KARVLAEA 9
KARVLAEA 365
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    28, Last sequence update)
    41, Last annotation update)
    [Contains: Core proteins P17,

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                                                                      Score 35;
Pred. No
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CORE PROTEIN P2.
CORE PROTEIN P7
CORE PROTEIN P1.
CORE PROTEIN P6.
                                                                                                                                          CCHC-TYPE
                                                                                                               YRISTATE (BY SIMILARITY)
023CA76C9C6F22AD CRC64;
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                                                        Mismatches
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PROTEIN P24
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No.
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16;
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                                                                                                                                                                                                    (NUCLEOCAPSID PROTEIN).
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                                                                                  Length 499;
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RESULT 9
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13-AUG-1987
01-FEB-1994
15-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00098; Zf-CCHC; 2.

Pfam; PF00540; Gag_p17; 1.

Pfam; PF00607; Gag_p2.

PRINTS; PR00939; CZHCZNFINGER.

PRINTS; PR00234; HIVIMATRIX.
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                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AIDS; Core protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00343; ZnF_C2HC;
PROSITE; PS50158; ZF_CCHC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIV; K03454; GAG$ELI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; K03454; AAA44324.1; -. EMBL; A07108; CAA00611.1; -. HSSP; P05888; 1AAF.
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-1- FUNCTION: PERFO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus type 1 (ELI isolate) (HIV-1). Viruses; Retroid viruses; Retroviridae; Lentivirus.
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InterPro; IPR000071; Retrovir_p17.
InterPro; IPR001878; Znf_CCHC.
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                                                                                                            Local
                                           2 KARVLAEA 9
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  KARVLAEA 365
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CCHC-TYPE
                                                                                                            Score 35;
Pred. No.
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E PROTEIN P2.
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                                                                                                                                                                                                                                                                                                                          (NUCLEOCAPSID PROTEIN).
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                                                                                                                                                                                                                                                                                                                                                                      (MATRIX PROTEIN) (CORE ANTIGEN).
                                                                                                                                  Length 499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P2,
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GAG_HV1H2
AC P0459
AC P0469
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Best Local S
Matches B
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InterPro; IPR001878; Znf_CCHC.
Pfam; PP00098; Zf-CCHC; Z.
Pfam; PF00540; Gag_p17; 1.
Pfam; PF00607; Gag_p24; 1.
Pfam; PF00607; Gag_p24; 1.
PRINTS; PR00334; HYVIMATRIX.
SMART; SM00343; ZnF_C2HC; Z.
                                                                                                                                                                                                                                             ZN_FING
                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AIDS Res. Hum. Retroviruses 3:57-69(1987).

-I- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL ASSEMBLY, THE PROTEINS FORM MEDICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY RESULT IN BUDDING OF AN IMMATURE VIRTON FROM THE INFECTED CELL. GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.

-I- PTM: THE P24 PROTEIN IS PHOSPHORYLATED.

-I- SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAG_HV1H2
P04591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=87299196; PubMed=3040055;
Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H.,
Gallo R.C., Wong-Staal F.;
                                                                                                                                                                                                                        TIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AIDS; Core p:
Zinc-finger;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUN-2002 (Rel. 41, Last annotation update)
GAG polyprotein [Contains: Core proteins P17, P24, P2, P7, P1, P6].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-AUG-1987 (Rel. 05, Created)
01-FEB-1994 (Rel. 28, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00343; ZnF_C2HC; 2.
PROSITE; PS50158; ZF_CCHC; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P05888; 1AAF.
HIV; K03455; GAG$HXB2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR000721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete nucleotide sequences of functional clones of the AIDS
358 KARVLAEA 365
                                              N
                         KARVLAEA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       K03455; AAB50258.1;
                                                                                            B; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein;
                                                                                                                                                                                                 499
                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Repeat.
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362
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Cnf_CCHC.
                                                                                                                                                                                              55798
                                                                                                                    79.5%;
100.0%;
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                                                                                                                    Score 35;
Pred. No.
                                                                                                                                                                                            CCHC-TYPE 1.
CCHC-TYPE 2.
CCHC-TYPE 2.
MYRISTATE (BY SIMILARITY).
774C384D6EACB108 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
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GAG_HVIJ3
GAG_HVIJ3
P12494;
01-OCT-1989 (Rel. 12, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-Jun-2002 (Rel. 41, Last annotation update)
15-21vorotein [Contains: Core proteins P17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHV1J3
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ZN_FING
LIPID
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CHAIN
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AIDS Res. Hum. Retroviruses 5:411-419(1989).

AIDS Res. Hum. Retroviruses 5:411-419(1989).

FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM MEMBRANE ASSOCIATIONS AND SELEF-ASSOCIATIONS THAT ULTIMATELY RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL. GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.

1- PTM: THE P24 PROTEIN IS PHOSPHORYLATED.

5-1- SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO0939; C2HCZNFINGE PRINTS; PRO0234; HIV1MATRIX SMART; SM00343; ZnF_C2HC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00540; Gag_p17; 1. Pfam; PF00607; Gag_p24; 1. PRINTS; PR00939; C2HCZNFINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000721; Gag_p24.
InterPro; IPR000071; Retrovir_p17.
InterPro; IPR001078; Znf_CCHC.
Pfam; PF00098; Zf-CCHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M21137; AABO3522.1;
HSSP; P05888; 1AAF.
HIV; M21137; GAG$JH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation - the European Bioinformatics institute. There are no restrictions on its
                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                       AIDS; Core protein;
Zinc-finger; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00343; ZnF_C2HC; PROSITE; PS50158; ZF_CCHC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus type 1 (JH3 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
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"Nucleotide sequences of gag and env genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=89352108; PubMed=2669897;
     Similarity
8; Conser
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     Conservative
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Polyprotein; Myristate; Phosphorylation;
                                                                                                     55725
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                                                     79.58;
                                                                                      CORE PROTEIN P24 (CORE PROTEIN P2.
CORE PROTEIN P7 (NUCLEOCAPSID CORE PROTEIN P1.
CORE PROTEIN P6.
CCHC-TYPE 1.
CCHC-TYPE 1.
CCHC-TYPE 2.
MYRISTATE (BY SIMILARITY).
*>P28112D4424AEE9 CRC64;
                                                                                                     XE:
                                                Score 35;
                                                                                                                                                                                                                                                                                                                          BY SIMILARITY CORE PROTEIN I
                           Pred.
     red. No. 16
Mismatches
                                                                                                                                                                                                E PROTEIN P17
E PROTEIN P2.
E PROTEIN P2.
E PROTEIN P7 ()
E PROTEIN P1.
E PROTEIN P6.
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                                                     B
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                                                                                                                                                                                                                                                   (NUCLEOCAPSID PROTEIN).
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E a Japanes
     0;
                                                                                                                                                                                                                                                                                                (MATRIX PROTEIN) (CORE ANTIGEN).
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                                                     Length 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    urimura T., Yoshida M.;
Japanese isolate of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P2,
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     Gaps
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2 KARVLAEA 9 |||||||| | 358 KARVLAEA 365

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                                                 Query Match
Best Local
                                                                                                                                                                                                              InterPro; IPR000071; Retrovir_p1
InterPro; IPR001878; Znf_CCHC.
Pfam; PF00098; zf-CCHC; 2.
Pfam; PF00540; Gag_p17; 1.
Pfam; PF00607; Gag_p24; 1.
Pfam; PF00607; Gag_p24; 1.
PRINTS; PR00939; CZHCZNFIKGER.
PRINTS; PR00939; CZHCZNFIKGER.
PRINTS; PR00934; HIVIMATRIX.
SMART; SM00343; ZnF_C2HC; 2.
PROSITE; PS50158; ZF_CCHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HV11W
                                                                                         ZN_FING
ZN_FING
LIPID
                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus type 1 (LW12.3 isolate) (HIV-1). Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
GAG polyprotein [Contains: Core proteins P17,
                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                      EMBL; U12055;
HSSP; P05888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q70622;
15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAG_HV1LW
                                                                               SEQUENCE
                                                                                                                         CHAIN
                                                                                                                                                      CHAIN
                                                                                                                                                                                                       AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=82834;
 358
                                                                                                                                                                                    INIT_MET
                                                                                                                                                                                            Zinc-finger;
                                                                                                                                                                                                                                                                                                          InterPro; IPR000721; Gag_p24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95127297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                    2 KARVLAEA 9
KARVLAEA 365
                                                                                                                                                                                                        Core
                                                                                                                                                                                                                                                                                                                               U12055; AAA76686.1; -
                                      8; Conserv
                                                                                                                                                                                                      protein;
                                                                               499
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362
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                                                                               55772
                                                 79.5%;
100.0%;
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CORE PROTEIN P24 (
CORE PROTEIN P2.
CORE PROTEIN P7 (
CORE PROTEIN P1 (
CORE PROTEIN P1.
CORE PROTEIN P6.
                                                 Score 35;
Pred. No.
                                                                              MYRISTATE (BY SIMILARITY)
AA2F683546EDC0A9 CRC64;
                                                                                                CCHC-TYPE 2.
                                                                                                             CCHC-TYPE
                                                                                                                                                                                    BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      499
                                                 16;
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                                                          1;
                                                                                                                                          (NUCLEOCAPSID PROTEIN).
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                                      0;
                                                                                                                                                             (MATRIX PROTEIN).
                                                          Length 499
                                       Indels
                                      0;
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RESULT 14
GAG_HV1Y2
ID GAG_I
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GAG_HV1N5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00098; Zf-CCHC; 2.
Pfam; PF00540; Gag_D17; 1.
Pfam; PF00607; Gag_D24; 1.
PRINTS; PR00939; C2HCZNFINGER.
PRINTS; PR00234; HIVIMATRIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M19921; AAA44987.1; -.
HISSP; P05888; 1AAF.
HIV; M19921; GAG$RL43.
InterPro; IPR000721; Gag_p24.
InterPro; IPR000071; Retrovir_p17.
InterPro; IPR001878; Znf_CCHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (CLONE PNL4-3).
Buckler C.E., Buckler-White A.J., Willey R.L., McCoy J.;
Submitted (JUN-1988) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-2002 (Rel. 41, Last annotation update) GAG polyprotein [Contains: Core proteins P17,
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Zinc-finger; Repeat
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PROSITE; PS50158; ZF_CCHC; 2.
AIDS; Core protein; Polyprotein; Myristate; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
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                                                                                                                         358 KARVLAEA 365
                                                                                                                                                  2 KARVLAEA
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PTM: THE P24 PROTEIN IS PHOSPHORYLATED.

SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
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8; Conserv
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Pred. No.
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MYRISTATE (BY SIMILARITY).
C8ECC1302FE2C1E2 CRC64;
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CORE PROTEIN I
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P24 (CORE ANTIGEN).
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GAG_HV1Y2

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Best Local :
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InterPro; IPR00071; Retrovit_p17.
InterPro; IPR001878; Znf_CCHC.
InterPro; IPR001878; Znf_CCHC.
Pfam; PF00098; Zf-CCHC; 2.
Pfam; PF00540; Gag_p17; 1.
Pfam; PF005607; Gag_p24; 1.
Pfam; PF000540; Gag_p24; 1.
Pfam; PF000343; GAG_CCHC; 2.
PROSITE; PR00234; HIVIMATRIX.
SMART; SM00343; ZnF_CCHC; 2.
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01-JUN-1994 (Rel. 29, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
GAG polyprotein (Contains: Core proteins P17, P24, P2,
                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                              AIDS; Core protein; |
Zinc-finger; Repeat.
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CORE PROTEIN P27 (MA
CORE PROTEIN P24 (CC
CORE PROTEIN P7 (NU
CORE PROTEIN P7 (NU
CORE PROTEIN P6.
CORE PROTEIN P6.
CCHC-TYPE 1.
CCHC-TYPE 2.
WYRISTATE (BY SIMILA
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                                                                                            Score 35;
Pred. No.
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InterPro; IPR000721; Retrovir_p17.
InterPro; IPR001878; Znf_CCHC.
Pfam; PF00098; Zf-CCHC; 2.
Pfam; PF00540; Gag_p17; 1.
Pfam; PF00540; Gag_p24; 1.
Pfam; PF00607; Gag_p24; 1.
PRINTS; PR00939; C2HCZNFINGER.
PRINTS; PR00939; HYUNATRIX.
SMART; SM00343; ZnF_C2HC; 2.
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SEQUENCE
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P12495;
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                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M22639; AAA45365.1; HSSP; P05888; 1AAF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus type 1 (Z2/CDC-Z34 isolate) (HIV-1). Viruses; Retroid viruses; Retroviridae; Lentivirus.
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01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
GAG polyprotein [Contains: Core proteins P17,
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INIT_MET 0
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PTM: THE P24 PROTEIN IS PHOSPHORYLATED.
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CORE PROTEIN P6.
CCHC-TYPE 1.
CCHC-TYPE 1.
CCHC-TYPE 2.
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US-09-989-735-373
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Sequence 804, App Sequence 4, Appli Sequence 4, Appli Sequence 7, Appli Sequence 347, App Sequence 2593, App Sequence 2593, App Sequence 372, App Sequence 373, App
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/09925299 Acids, Proteins and	\$/09925299 17A9 17A9 c Acids, Proteins and us/09/925,299 -08-10 PCT/US00/05883 -08 60/124,270 -12 0 0 68; Score 35; DB 9; 08; Pred. No. 25; 08; Pred. No. 25; 08; Pred. No. 25;	ALIGNMENTS	US-09-989-734-37 US-10-028-072-47 US-10-028-072-47 US-09-997-663-37 US-10-112-049-47 US-10-1140-470-47 US-10-140-470-47 US-09-990-438-37 US-09-997-666-37 US-09-997-666-37 US-10-176-918-47 US-10-176-918-47 US-10-176-918-47 US-10-140-474-47 US-10-140-474-47 US-10-140-474-47 US-10-140-474-47 US-10-140-474-47 US-10-140-474-47 US-10-140-474-47 US-10-140-474-47 US-10-140-474-47 US-10-140-474-47 US-10-140-474-47 US-10-140-474-47 US-10-140-474-47 US-10-140-474-47 US-10-140-474-47 US-10-140-474-474-474-474-474-474-474-474-474-4
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CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883

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US-09-957-485-4
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US-09-987-021-4
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                                                                                          Sequence 4, Application US/09957485 Patent No. US20020143165A1 GENERAL INFORMATION:
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Best Local Similarity /v.v.
"---hes 7; Conservative
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PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PALENTIN VET. 2.0
SEQ ID NO 804
LENGTH: 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. SEQ ID NO 4
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Best Local :
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                                APPLICANT: Human Genome Sciences, Inc. et al.
TITLE OF INVENTION: Brain-Associated Inhibitor
TITLE OF INVENTION: Activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/987,021 CURRENT FILING DATE: 2001-11-13
                   FILE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 08/948,997 PRIOR FILING DATE: 1997-10-10 PRIOR APPLICATION NUMBER: 60/028,117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Brain-Associated Inhibitor of Tissue-Type Plasminogen Activator FILE REFERENCE: PF336P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 09/722,292
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 60/247,971
PRIOR FILING DATE: 2000-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: 09/957,485
PRIOR FILING DATE: 2001-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/123,704 PRIOR FILING DATE: 1999-03-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/521,664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 09/348,817 PRIOR FILING DATE: 1999-07-08
                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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                   REFERENCE:
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NUMBER: US/09/957,485
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70.08;
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70.0%;
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Pred. No.
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Pred. No.
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                                                 of Tissue-Type Plasminogen
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GENERAL INFORMATION:
APPLICANT: Meyers, Rachel A.
TITLE OF INVENTION: 26443 and 46873, NOVEL HUMAN
TITLE OF INVENTION: ASPARAGINASE FAMILY MEMBERS AND USES THEREFOR
FILE REFERENCE: 10448-029001
CURRENT APPLICATION NUMBER: US/09/816,664
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 60/191,973
PRIOR APPLICATION NUMBER: US 60/191,973
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 9
SOCTWARR: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 378
TYPE: PRT
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Best Local Similarity
Thes 7; Conserve
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US-10-101-464A-75
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                                                                                                                                                                                     Sequence 75, Application US/10101464A Publication No. US20030046728A1 GENERAL INFORMATION:

APPLICANT: Strabala, Timothy APPLICANT: Nieuwenhuizen, Nicolaas APPLICANT: Higgins, Colleen M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US Patent No. US20020038014A1
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             CURRENT APPLICATION NUMBER: US/10/101,464A CURRENT FILING DATE: 2002-03-18 PRIOR APPLICATION NUMBER: 09/704,302 PRIOR FILING DATE: 2000-11-01 PRIOR APPLICATION NUMBER: 09/228,986 PRIOR APPLICATION NUMBER: 09/228,986 PRIOR FILING DATE: 1999-01-12
                                                                                                                               TITLE OF INVENTION: Compositions Isolated TITLE OF INVENTION: and Their Use in the FILE REFERENCE: 11000.1020c2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: US 09/521,664
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: US 60/123,704
PRIOR FILING DATE: 1999-03-10
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver: 2.1
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TYPE: PRT
ORGANISM: Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                     162 DISTFETQE 170
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APPLICATION NUMBER: 60/162,866
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Pred. No.
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Modification
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Query Match
Best Local Similarity
Tatches 6; Conserve
                                NUMBER OF SEQ ID NOS: 2606
SOFTWARE: Corixa Invention Disclosure Database SEQ ID NO 2593
LENGTH: 1531
TYPE: PRT
ORGANISM: Homo sapiens
US-09-998-598-2593
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Best Local Similarity
7; Conserve
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: SOFTWARE: FastSEQ for Windows Version 4.0
: SEQ ID NO 75
: LENGTH: 659
: TYPE: PRT
: ORGANISM: Eucalyptus grandis
US-10-101-464A-75
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                                                                                                                                                                                    Sequence 2593, Application US/09998598
Patent No. US20020150922A1
GENERAL INFORMATION:
APPLICANT: Stolk, John A.
APPLICANT: Chenault, Ruth A.
APPLICANT: Meagher, Madelein Joy
APPLICANT: Meagher, Madelein Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.561
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CURRENT FILING DATE: 2001-06-06
NUMBER OF SEQ ID NOS: 353
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 347
LENGTH: 1531
TYPE: PRT
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Query Match
                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/998,598
CURRENT FILING DATE: 2001-11-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR OVARIAN TITLE OF INVENTION: CANCER THERAPY AND DIAGNOSIS FILE REFERENCE: 210121.466C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Benson, Darin R.
APPLICANT: Lodes, Michael J.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
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PRIOR FILING DATE: 2000-01-11
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Pred. No.
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Pred. No.
Score 33;
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DB 10;
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Length 1531;
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -34..-1
US-09-731-872-352
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US-09-318-271-2
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LENGTH: 314
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 352, Application Patent No. US20020102604A1 GENERAL INFORMATION:
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Matches 7; Conserva:
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LENGTH: 206
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TITLE OF INVENTION: "VITAMIN C PRODUCTION IN MICROORGANISMS AND PLANTS"
FILE REFERENCE: 3161-24
CURRENT APPLICATION NUMBER: US/09/318,271A
CURRENT FILING DATE: 1999-05-25
EARLIER APPLICATION NUMBER: 60/125,073
EARLIER FILING DATE: 1999-03-17
EARLIER FILING DATE: 1999-03-17
EARLIER FILING DATE: 1999-03-18
EARLIER APPLICATION NUMBER: 60/125,054
EARLIER FILING DATE: 1999-03-18
EARLIER FILING DATE: 1999-03-18
EARLIER APPLICATION NUMBER: 60/088,549
EARLIER FILING DATE: 1999-03-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
Query Match
Best Local Similarity
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APPLICANT: Running, Jeffrey A
APPLICANT: Severson, David K.
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bougueleret, Lydie
APPLICANT: Jobert, Severin
TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
FILE REFERENCE: 78.US3.REG
                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 482
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/169,629
PRIOR FILING DATE: 1999-12-08
PRIOR APPLICATION NUMBER: US 60/187,470
PRIOR FILING DATE: 2000-03-06
                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 2000-12-07
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                                                                                                                                                 TYPE: PRT
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5. US20020012979A1
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                                                           SOFTWARE: PatentIn Ver.
                                                                                   PRIOR FILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 09/154,707 PRIOR FILING DATE: 1998-09-17
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OR FILING DATE: 1997-05-30
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FILING DATE: 1997-05-30
APPLICATION NUMBER: US 60/048,154
FILING DATE: 1997-05-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/041,276 FILING DATE: 1997-03-21 APPLICATION NUMBER: US 60/041,281 FILING DATE: 1997-03-21 APPLICATION NUMBER: US 60/048,094 FILING DATE: 1997-05-30 APPLICATION NUMBER: US 60/048,094 APPLICATION NUMBER: US 60/041,276 APPLICATION NUMBER: US 60/041,276 APPLICATION NUMBER: US 60/041,276 APPLICATION NUMBER: US 60/041,281 APPLICATION NUMBER: US 60/048,094 AP
                                                                                                                                               APPLICATION NUMBER: US 60/060,862
                                                                                                                                                                          FILING DATE: 1997-08-19
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US-09-992-598-373
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PRIOR FILLING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILLING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILLING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILLING DATE: 1997-11-24
PRIOR FILLING DATE: 1997-11-24
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CURRENT APPLICATION NUMBER: US/09/992,598

CURRENT FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/
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80 ADLSSLKS 87
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                                                                                                                                                                       APPLICATION NUMBER: 60/
FILING DATE: 1998-05-28
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                                                        FILING DATE: 1998-06-02
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Stewart, Timothy A.
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Gerritsen, Mary E.
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PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C66
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APPLICATION NUMBER: 60/087827
FILING DATE: 1998-06-03
APPLICATION NUMBER: 60/088021
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APPLICATION NUMBER: 60/084600
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Williams, P. Mickey
Wood, William I.
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Kljavin, Ivar J.
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                        ADLSSFKS 8
ADLSSLKS 100
                                                  . Similarity
7; Conserv
                                                  Conservative
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                                                 Score 31; DB Pred. No. 93; 0; Mismatches
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                                                                          Length 229;
                                                  Indels
                                                  0,
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RESULT 14

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CURRENT APPLICATION NUMBER: US/09/989,735
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
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OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/08322
OR FILING DATE: 1998-04-28
OR APPLICATION NUMBER: 60/084600
OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/087106
OR FILING DATE: 1998-05-28
OR APPLICATION NUMBER: 60/087607
OR FILING DATE: 1998-06-02
OR APPLICATION NUMBER: 60/087609
OR APPLICATION NUMBER: 60/087769
OR APPLICATION NUMBER: 60/087759
                                           DR APPLICATION NUMBER: 60/088025
DR FILING DATE: 1998-06-04
DR APPLICATION NUMBER: 60/088026
DR FILING DATE: 1998-06-04
DR APPLICATION NUMBER: 60/088029
DR APPLICATION NUMBER: 60/088029
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FILING DATE: 1998-06-04
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FILING DATE: 1997-11-13
APPLICATION NUMBER: 60/
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Williams, P. Micke
Wood, William I.
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Stewart, Timothy A.
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Gurney, Austin L.
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b. US20020193299A1
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APPLICATION FILING DATE:

NUMBER: 60/ : 1998-06-04

60/088033

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RESULT 15
US-09-990-444-373
Sequence 373, Application US/09990444
Publication No. US20020193300A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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Best Local S
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OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/090472
OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/090535
OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/090540
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OR APPLICATION NUMBER: 60/09057
OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/090676
OR FILING DATE: 1998-06-25
OR APPLICATION NUMBER: 60/090676
OR FILING DATE: 1998-06-25
OR APPLICATION NUMBER: 60/090690
OR FILING DATE: 1998-06-25
OR APPLICATION NUMBER: 60/090694
OR FILING DATE: 1998-06-25
OR APPLICATION NUMBER: 60/090695
OR APPLICATION NUMBER: 60/090696
OR FILING DATE: 1998-06-25
OR APPLICATION NUMBER: 60/090863
OR APPLICATION NUMBER: 60/090863
OR APPLICATION NUMBER: 60/091863
OR APPLICATION NUMBER: 60/091863
OR APPLICATION NUMBER: 60/091478
OR APPLICATION NUMBER: 60/091478
OR APPLICATION NUMBER: 60/09154
OR APPLICATION NUMBER: 60/091526
OR APPLICATION NUMBER: 60/09163
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OR APPLICATION NUMBER: 60/090429
OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/090431
OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/090435
OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/090444
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FILING DATE: 1998-07-07
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Pred. No. 93;
0; Mismatches
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OR APPLICATION NUMBER: 60/088326
OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/088326
OR ETLING DATE: 1998-06-05
OR APPLICATION NUMBER: 60/088202
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OR APPLICATION NUMBER: 60/088212
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OR APPLICATION NUMBER: 60/088734
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OR FILING DATE: 1998-06-10
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OR APPLICATION NUMBER: 60/088826
OR FILING DATE: 1998-06-11
OR APPLICATION NUMBER: 60/088858
OR FILING DATE: 1998-06-11
OR APPLICATION NUMBER: 60/089826
OR APPLICATION NUMBER: 60/089512
OR APPLICATION NUMBER: 60/089514
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OR APPLICATION NUMBER: 60/089600
OR FILING DATE: 1998-06-17
OR APPLICATION NUMBER: 60/089653
OR FILING DATE: 1998-06-17
OR APPLICATION NUMBER: 60/089801
OR FILING DATE: 1998-06-18
OR APPLICATION NUMBER: 60/089907
OR FILING DATE: 1998-06-18
OR APPLICATION NUMBER: 60/089908
OR APPLICATION NUMBER: 60/089908
OR FILING DATE: 1998-06-19
OR APPLICATION NUMBER: 60/089947
OR FILING DATE: 1998-06-19
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R APPLICATION NUMBER: 60/09
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60/090349 60/090254 60/090252 60/090246 60/089952

APPLICATION NUMBER: 60/1 FILING DATE: 1998-06-19

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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OR FILING DATE: 1998-04-28
OR APPLICATION NUMBER: 60/084600
OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/087106
OR FILING DATE: 1998-05-28
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OR FILING DATE: 1998-06-02
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FILING DATE: 1997-10-17
APPLICATION NUMBER: 60/065186
FILING DATE: 1997-11-12
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APPLICATION NUMBER: 60/088033
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088326
FILING DATE: 1998-06-04
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ETILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087759
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    APPLICATION NUMBER: 60/
FILING DATE: 1998-06-05
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Gerber, Hanspeter
Gerritsen, Mary E.
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OR APPLICATION NUMBER: 60/088861
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OR APPLICATION NUMBER: 60/089105
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OR APPLICATION NUMBER: 60/089532
OR FILING DATE: 1998-06-17
OR APPLICATION NUMBER: 60/089538
OR FILING DATE: 1998-06-17
OR APPLICATION NUMBER: 60/089599
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OR APPLICATION NUMBER: 60/089653
OR FILING DATE: 1998-06-17
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OR APPLICATION NUMBER: 60/089907
OR FILING DATE: 1998-06-18
OR APPLICATION NUMBER: 60/089908
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OR APPLICATION NUMBER: 60/089947
OR FILING DATE: 1998-06-19
OR APPLICATION NUMBER: 60/089952
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OR APPLICATION NUMBER: 60/090254
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    NUMBER: 60/090435
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OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/088810
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APPLICATION NUMBER: 60/088212
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APPLICATION NUMBER: 60/088217
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PRIOR RILLANION NUMBER: 60/990444
PRIOR RILLA DATE: 1998-60-24
PRIOR RILLA DATE: 1998-60-25
PRIOR REPLICATION WINDER: 60/990472
PRIOR PLICATION WINDER: 60/990472
PRIOR PLICATION WINDER: 60/990472
PRIOR PLICATION WINDER: 60/990472
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                                        Query Match
Best Local S
Matches 11
                                                                                                                          TELEPHONE: (515) 288-3667
TELEPAX: (515) 288-1338
INFORMATION FOR SED ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
                                                                                                                                                                  APPLICATION NUMBER: US/08/365
FILING DATE: 28-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Nebel, Heidi S.
REGISTRATION NUMBER: 37,719
REFERENCE/DOCKET NUMBER: Uirf
TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 288-3667
                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 14 MCLINGS OF ADDRESSE: ADDRESS: ADDRESSE: Zarley, McKee, Thomte, STREET: 801 Grand Ave. Suite 3200 CITY: Des Moines
STATE: Iowa
                                                                                             TOPOLOGY: 11
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TITLE OF INVENTION: and Methods of Use for Same
NUMBER OF SEQUENCES: 14
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APPLICANT: Nunez, Raphael D.
APPLICANT: Yodoi, Jungi
                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
79
                                                                                                                   TYPE:
                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                    COMPUTER:
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SYSTEM: PC-DOS/MS-DOS
                                                                                                         linear
                                                                                             protein
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US-08-394-177-5
US-08-394-912A-5
US-09-33-636-5
US-09-147-236-5
US-09-147-236-5
US-09-147-236-5
US-09-134-001C-5016
US-09-134-001C-4059
US-08-800-682-3
US-09-221-235-5
US-09-221-235-5
US-09-221-236-5
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                                                   Score 51; DB 1;
Pred. No. 0.011;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Issued_Patents_AA:*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Minimum DB Maximum DB

seq length:
seq length:

2000000000

Total number of hits satisfying chosen parameters:

Title: Perfect score:

US-10-050-200-4

Run on: Š

protein -

protein search, using sw model

GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

March 13, 2003, 18:46:52; Search time 9.8 Seconds (without alignments) 33.026 Million cell updates/sec

Scoring table: Sequence:

BLOSUM62

Gapop 10.0 , Gapext 0.5

262574 seqs, 29422922 residues

Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

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US-08-365-103B-12

GENERAL INFORMATION:

Application US/08365103B

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                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-365-103B-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 51; Best Local Similarity 100.0%; Pred. No. Matches 11; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10,
                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION: APPLICANT: Lynch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (515) 288-3667
TELEFAX: (515) 288-1338
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 167 amino acids
                                                                                                                                                                                              APPLICANT: Lynch, Richard G
APPLICANT: Nunez, Raphael D.
APPLICANT: Yodol, Jung1
TITLE OF INVENTION: DNA Sequences for Soluble Froms of CD23
TITLE OF INVENTION: and Methods of Use for Same
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,103B
FILING DATE: 28-DEC-1994
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS_MS-DOS
SOFTMARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Nebel, Heldi S.
REGISTRATION NUMBER: 37,719
REFERENCE/DOCKET NUMBER: Ulrf N5-24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 288-3667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Yodo1, Jung1
TITLE OF INVENTION: DNA Sequences for Soluble Froms of CD23
TITLE OF INVENTION: and Methods of Use for Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Lynch, Richard G
APPLICANT: Nunez, Raphael D.
                                                                                                                  CITY: Des Moines
STATE: Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Zarley, McKee, Thomte, Voorhees & Sease
STREET: 801 Grand Ave. Suite 3200
CITY: Des Moines
                                                                       COUNTRY: UZIP: 50309
                                                                                                                                                           STREET:
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                                                                                                                                                                                                                                                                                                                                                                                       0, Application US/08365103B 5766943
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                                                                                                                                                           E: Zarley, MCKee, Thomte, Voorhees & Sease
801 Grand Ave. Suite 3200
                                                                                         United States
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Query Match

100.0%; Score 51;

DB 1;

Length 321;

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US-08-365-103B-8
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                                                                                   TELEFAX: (515) 288-1338 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (515) 288 1338
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Nebel, Heldi S.
REGISTRATION NUMBER: 37,719
REFERENCE/DOCKET NUMBER: Uirf
TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 288-3667
                                                                                                                                                         APPLICATION NUMBER: US/08/365
FILING DATE: 28-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Nebel, Heid1 S.
REGISTRATION NUMBER: 37,719
REFERENCE/DOCKET NUMBER: Uirf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,103B
                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (515) 288-3667
                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: DNA Sequences for Soluble Froms of CD23
TITLE OF INVENTION: and Methods of Use for Same
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 320 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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CURRENT APPLICATION DATA:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 ADLSSFKSQEL 127
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CITY: Des Moines
STATE: Iowa
            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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                                                LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                               50309
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                             : 321 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/08365103B
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801 Grand Ave. Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lyncn, Richard G
Nunez, Raphael D.
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US-09-348-817A-4
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                                                                                                                          Sequence 4, Application US/09348817A
Patent No. 6191260
GENERAL INFORMATION:
APPLICANT: Hastings et al
                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08948997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100 Matches 11; Conservative
FILE REFERENCE: PF336D1
CURRENT APPLICATION NUMBER: US/09/348,817A
CURRENT FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: 08/948,997
PRIOR FILING DATE: 1997-10-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                        TITLE OF INVENTION: Brain-Associated Inhibitor of Tissue-Type Plasminogen TITLE OF INVENTION: Activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: COLEMAN, TIM
APPLICANT: LAWRENCE, DANIEL
TITLE OF INVENTION: TISSUE-TYPE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/948,997
FILING DATE: Oct-10-97
CLASSIFICATION: 4-5
ATTORNEY/AGENT INFORMATION:
NAME: A. ANDERS BROOKES
REGISTRATION NUMBER: 36,373
REGERENCY/COURTE NUMBER: 36,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: HASTINGS, GREGG
                                                                                                                                                                                                                                                                     327 ADFSSFSDQE 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
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9410 KEY WEST AVENUE
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70.0%;
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                                                                                                            ; MOLECULE TYPE: US-08-261-825-2
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US-08-261-825-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-348-817A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Appril 10, 5558993
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SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best
                                                       Matches
                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                  TELEFAX: (619) 455-5110 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 402
TYPE: PRT
ORGANISM: Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: APPLICANT:
                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acid
                                                                                                                                                                                                                                           REGISTRATION NUMBER: P-38,3
REFERENCE/DOCKET NUMBER: PD
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                  FILING DATE: 17-JUN-1994
FILING DATE: 17-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: TUMARKIN, LISA A. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: LOS Angeles
CITY: LOS Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: CLONED I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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                                                                     Local
17
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/261,825 FILING DATE: 17-JUN-1994
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                         2 DLSSFKSQEL 11
DLSAFMSQDI 26
                                                      Similarity
6; Conserve
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                                                                                                                                                      amino acid
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                                                                                                                                                                    174 amino acids
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1880 Century Park East, Suite 500
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Blanco, David R.
WENTION: CLONED Borrelia burgdorferi VIRULENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lovett, Michael A. Haake, David A.
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                                                       Conservative
                                                                                                                                            linear
                                                                                                                                                                                                                                (619) 455-5100
                                                                                                                           protein
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                                                                     64.7%;
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Pred. No.
                                                                   Score 33; DB 1; Length 174; Pred. No. 35;
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                                                       Mismatches
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RESULT 8

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RESULT 9
PCT-US95-07748A-2
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GENERAL INFORMATION:
APPLICANT: The Re
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APPLICATION NUMBER: 08/261,825
FILING DATE: 17-JUN-1994
ATTORNEY/ACENT INFORMATION:
NAME: TUMARKIN, LISA A.
REGISTRATION NUMBER: P-38,347
REFERENCE/DOCKET NUMBER: PD3516
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
                                                                                                                                                           TITLE OF INVENTION: CLONED E TITLE OF INVENTION: PROTEIN NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICANT: Blanco, David R.
TITLE OF INVENTION: CLONED Borrelia burgdorferi VIRULENCE
TITLE OF INVENTION: PROTEIN
                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                   CITY: La Jolla
STATE: California
COUNTRY: USA
                                                                                                                           STREET:
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les 6; Conservat
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STATE: California
                                                                                                                                              ADDRESSEE:
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   COMPUTER:
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                                                                                                                           4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Spensley Horn Jubas & Lubitz
1880 Century Park East, Suite 500
                                                                                                                                                                                                                    The Regents of the University of California VENTION: CLONED Borrelia burgdorferi VIRULENCE
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Haake, David A.
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IBM PC compatible
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Pred. No. 35;
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Sequence 1, Application US/08889402
Patent No. 5811288
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL ISOFORM
TITLE OF INVENTION: PROTEIN PAXILI
NUMBER OF SEQUENCES: 7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity
Friches 6; Conserve
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US-08-889-402-1
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; ORGANISM: Eucalyptus grandis
US-09-228-986-75
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Best Local Similarity
"~+~hes 6; Conserv?
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 75
LENGTH: 659
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Patent No. 6359198
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: Compositions Isolated from Plant Cell Signalling
FILE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
FILE REFERENCE: 11000/1020
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT FILING DATE: 1999-01-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (619) 678-5099
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07748A
FILING DATE: 16-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: HAILE, Ph.D., LISA A.
                                                                                                                                                                                                                                                                                             289 DVATEKHQEL 298
           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
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                                                                                                                                                                                                                                                                                                                             2 DLSSFKSQEL 11
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                   Score 33; DB 4;
Pred. No. 1.4e+02;
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                 Version #1.30 (EPO)
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                                                              US-08-296-014A-4
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                Query Match
                                                                                                                                                   TELEFAX: (703) 205-80 TELEX: 248345 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: 7
TITLE OF INVENTION: 5
TITLE OF INVENTION: 1
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                           TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                             TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 271 ASLSDFKIODL 281
                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/296,014A FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Falls Church
STATE: Virginia
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                 Local
                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                       NAME: Murphy, Jr., Gerald M. REGISTRATION NUMBER: 28,977
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                                                                                                                       LENGTH:
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 Similarity 54.96; Conservative
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8110 Gatehouse Road, Suite 500 East
                                                                                                                       1019 amino acids
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                                                                                                                                                                               (703) 205-8050
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                                                                                                                                                                                                                                                                                        435
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                 62.7%;
54.5%;
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Score 32; DB 1; Le
Pred. No. 3.6e+02;
Pred. No. 3.6e+02;
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Pred. No.
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                                                                                                                                                        Patent No.
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                                                                                                                                                                       Sequence 4,
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                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                        GENERAL INFORMATION:
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TELEX: 248345
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: MUPPHy, Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1781-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Ko
STREET: 8110 Gatehouse Road,
                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                        APPLICANT: Ding, Je APPLICANT: Ho, Bow
                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1019 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
                                             NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                 Conservative
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                                                            The Cloned Factor C cDNA of the Singapore Horseshoe Crab, Carcinoscorpius rotundicauda and Purification of Factor C Proenzyme
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54.5%;
 Stewart, Kolasch & Birch
house Road, Suite 500 East
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Pred. No.
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. 3.6e+02;
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

STATE: Virginia

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GENERAL INFORMATION:
APPLICANT: Ding, Jeak Ling
APPLICANT: Ho, Bow
TITLE OF INVENTION: The Cloned Factor C cDNA of the
TITLE OF INVENTION: Singapore Horseshoe Crab, Carcinoscorpius
TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: B1rch, Stewart, Kolasch & Birch
STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-296-014A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;. MOLECULE TYPE: protein US-08-877-620-4

    Matches

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PRIOR APPLICATION UMBER: 08/596,405

FILING DATE:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
AREISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1781-105P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8000
TELEFAX: (703) 205-8050
TELEFX: 248345
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1019 amino acids
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5716834
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Best Local 9
APPLICATION NUMBER: US/08/296,014A FILING DATE:
CLASSIEFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MULTIPLY, Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1781-105P
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/877,620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 404 SDLNGIKSEEL 414
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TOPOLOGY: linear
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54.5%;
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Pred. No. 3.6e+02;
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Search completed: March 13, 2003, 18:53:51 Job time: 10.8 secs
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TELEX: 248345
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1083 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                        Query Match
                                                                                                                           Matches
                                                             468 SDLNGIKSEEL 478
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Local Similarity 54.5%;
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1 ADLSSFKSQEL 11
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Q9WMH6
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Q19542
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                 Q9pr79 ureaplasma
Q982f6 rhizobium 1
000805 leishmania
Q9vub0 drosophila
Q9vub0 drosophila
Q9vvf8 drosophila
Q9vvf8 drosophila
Q9wnf6 newcastle d
Q9wnb6 newcastle d
Q9fvy2 oryza sativ
084483 chlamydia t
031711 bacillus su
                                                                                                            Q9pjr6 chlamydia (Q9f0b9 lactobacil)
                                                                                                                               P90872 caenorhabdi
Q19542 caenorhabdi
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caenorhabdi
caenorhabdi
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176	150	149	149	149	108	108	81	1812	1526	1526	1320	712	701	694	694	507	458	388	265	263	209	205	193	174	142	142	142	75
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			Q8wsp7 halocynthia	001355 halocynthia	P78938 schizosacch	S	Q8s8n3 arabidopsis	097275 plasmodium	O55079 cricetulus	B	Q96kf5 homo sapien	Q9u2s0 caenorhabd1	Q92ea7 listeria in	pomo	homo	Q96k90 homo sapien			Q97ze4 sulfolobus	Q9xv47 caenorhabdi		Q8y9t5 listeria mo			0	7	718	Q38347 lactococcus

ALIGNMENTS

P90872 PRELIMINARY; PRT; 305 AA.
P90872; P90973;
01-MAY-1997 (TrEMBLrel. 03, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JAN-1999 (TrEMBLrel. 09, Last annotation update)

F39H2.3 protein.

F39H2.3

Caenorhabditis elegans. Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

SEQUENCE FROM N.A. NCBI_TaxID=6239;

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RESULT 1
P90872
ID P908
AC P01-1
A
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latrellle P.,
Jones M., Kershaw J., Komurray A., Mortimore B., O'Callaghan M.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen F.
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
                                                                                                                                                                                                                                                                                                                                                                              Watson
"2.2 M
SEQUENCE FROM N.A.

Kershaw J.;

Kershaw J.;

Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.

EMBL; Z81098; CAB03184.1; -.

EMBL; Z81080; CAB03184.1; JOINED.
                                                                                                                                                                                                                                                                               Nature 368:32-38(1994).
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Best Local S
Matches 8
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O9PJR6,
01-OCT-2000 (TrEMBLrel. 1
01-OCT-2000 (TrEMBLrel. 1
01-JUN-2002 (TrEMBLrel. 2
DNA methyltransferase.
TC0762.
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Q19542;
Q1-NOV-1996 (TrEMBLrel. C
01-NOV-1996 (TrEMBLrel. C
01-DEC-2001 (TrEMBLrel. 1
F18C12.1 protein.
SEQUENCE FROM N.A.
STRAIN-MOPN / NIGG;
MEDILINE-20150255, PubMed-10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg
White O., Hickey E.K., Peterson J., Utterback T., Berry
White N., Weidman J., Khouri H., Craven B., Bowman C.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G.,
Eisen J., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1515
                                                                                                                                                                                                                                                                  Chlamydia muridarum.
Bacteria; Chlamydiales;
NCBI_TaxID=83560;
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Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
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Science 282:2012-2018(1998).
EMBL; Z75536; CAA99830.1; -.
HSSP; P02632; ICB1.
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investigating biology.":
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Z81098; CAB03089.1;
NCE 305 AA; 34360
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8; Conservative
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Pred. No.
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                           g J.F.,
y K., Bass S.,
, Dodson R.,
, Salzberg S.L.,
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  Cassell G.H.;
"The complete s
urealyticum.";
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SEQUENCE FROM N.A.
STRAIN-SEROVAR 3;
MEDLINE-20500219; PubMed-11048724;
MEDLINE-10500219; PubMed-11048724;
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01-MAR-2001
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01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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                                                                                                                                                                                                  Ureaplasma parvum (Ureaplasma urealyticum biotype
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                           PTA OR UU066
                                                                                                                                                                                                                                                              Phosphotransacetylase.
                                                                                                                                                                                                                                                                                                                                                                 Q9PR79
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"EPS cluster of Lactobacillus delbrueckii subsp.
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ dai
EMBL; AF267127; AAG44713.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lactobacillus delbrueckii (subsp. bulgaricu
Bacteria; Firmicutes; Bacillus/Clostridium
Lactobacillaceae; Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001497; Methyltransf_1.
Pfam; PF01035; Methyltransf_1; 1.
TIGREAMS; TIGR00589; ogt; 1.
PROSITE; PS00374; MGMT; UNKNOWN_1.
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Nucleic Acids Res. 28:1397-1406(2000).
                                                                                                                                                         Mycoplasmataceae;
NCBI_TaxID=134821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-LF15
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7; Conser
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                    sequence
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                      mucosal
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                                                            J.S.,
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ostridium group; Lactobacillales;
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                    pathogen
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19;
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                                                            C.R.,
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                                                                                                                                                                                                      Mollicutes;
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EMBL; AE002106; AAF30471.1; -.
Interpro; IPR002505; PTA_PTB.
Pfam; PF01515; PTA_PTB; 1.
Complete proteome.
SEQUENCE 293 AA; 33369 MW;
                                                                                                                                         P-glycoprotein E.
Leishmania tropica.
Eukaryota; Euglenozoa;
                                                                                                                                                                                                                 000805;
01-JUL-1997 (TrEMBLrel.
01-JUL-1997 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bac Mesorhizobium loti.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q982F6;
01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=MAFF303099;
MEDLINE=21082930; PubMed=11214968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Phyllobacteriaceae; Mesorhizobium.
                           STRAIN-LRC-L39;
Lafuente E., Ca
                                                                                                                                                                                                                                                                                                                   000805
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                                                                        SEQUENCE FROM N.A.
                                                                                                                       NCBI_TaxID=5666;
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EMBL; AP003015; BAB54503.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                        289
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||||||: |:
48 DLSSFKTPEI 57
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les 8; Conserv
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  E., Castanys S. (APR-1996) to
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                                                                                                                                           Kinetoplastida;
., Gamarro F.;
the EMBL/GenBank/DDBJ databases
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21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the nitrogen-fixing symbiotic bacterium
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Last sequence update)
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Pred. No.
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                                                                                                                                              Trypanosomatidae; Leishmania
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RA Addams M.D., Celniker S.E., Li P.W., Hoskins R.A., Golayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Baxer E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Gepson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Gerry J.M., Cawley S., Dahlke C., Daveport L.B., Davies P.,
RA Gerry J.M., Cawley S., Dahlke C., Daveport L.B., Davies P.,
RA Gerry J.M., Cawley S., Dahlke C., Daveport L.B., Davies P.,
RA Gerry J.M., Cawley S., Dahlke C., Dunnov B.C., Petria C., Ferria C
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Best Local S
Matches 7
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01-MAY-2000 (Trew
01-JUN-2000 (Trew
CG17362 protein.
CG17362.
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Eukaryota; Metazoa; Arthropoda; Diptera; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc

Ephydroidea; Drosophilidae; Drosophila.
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InterPro; IPR001140; ABCtranprtrTM.
InterPro; IPR003439; ABCtransportr.
InterPro; IPR003439; ABCtransportr.
InterPro; IPR001865; Ribosomal_S2.
InterPro; IPR00504; RNA_rec_mot.
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1677 AA;
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PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20196006; PubMed=10731132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Pred. No. 1.8e+02;
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RESULT 10
Q9VVF8
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Best Local S
Matches 8
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RC STRAIN-C2A / ATCC 35395 / DSM 2834;

RX MEDLINE-21929760; PubMed-11932238;

RX MEDLINE-21929760; PubMed-11932238;

RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown R.,

RA Linton L., McEwan P., McKernen K., Talamas J., Tirrell A., Ye W.,

RA Linton L., McEwan P., McKernen K., Talamas J., Tirrell A., Ye W.,

RA Linton L., McEwan P., McKernen K., Talamas J., Tirrell A., Guss A.M.,

RA Linton L., McEwan P., McKernen K., Talamas J., Tirrell A., Guss A.M.,

RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,

RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,

RA Leigh J.A., Unayam L.A., White O., White R.H., de Macario E.C.,

RA Springer T.A., Unayam L.A., White O., White R.H., de Macario E.C.,

RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,

RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,

RA Pritchett M., Birren B.;

RT and physiological diversity.*;

Renome Res. 12:532-542(2002).
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Best Local S
Matches 7
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Q1-JUN-2002 (TrEMBLrel. 21, C
Q1-JUN-2002 (TrEMBLrel. 21, I
Q1-JUN-2002 (TrEMBLrel. 21, I
Hypothetical protein MA0641.
                                     Q9VVF8;
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EMBL; AE003536; AAAF49779,1; "EMBL; AE003536; AAAF49789,1; "ENGLENCE 183 AA; 19807 MW; BB6263A75679B9A2 CRC64;
 01-MAY-2000 (TremBLrel. 01-MAY-2000 (TremBLrel. 01-MAY-2000 (TremBLrel.
                                                                                                                                                                                 Genome Res. 12:534-3-1. Genome Res. 12:534-3-1. -.
EMBL; AE010726; AAM04083.1; -.
HYPOTHECICAL PROTEIN; Complete proteome.
HYPOTHECE 467 AA; 51705 MW; FE440724FBB90EBF CRC64;
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Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
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                                                  PRELIMINARY;
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72.7%;
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70.0%;
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Pred. No.
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Q9WMH6
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Ballew R.A., Galler R.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Baynektaroglu L., Beldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Baynektaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Charry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA Charry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA Charry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA Charry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA Charry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA Charry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA Clock R., Doup L.E., Downes M., Dugan-Rocha S., Dankov B.C., Dunn P.,
RA Clock R., Goog F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hortis N.L., Harvey D., Helman T.J., Hernandez J.R., Flouck J.,
RA Glodek A., Goog F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Harris M., Kallsh F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Harris M., Kallsh F., Karpen G.H., Ke Z., Mennison J.A., Ketchum K.A.,
RA Menkulov G., Milshina N.V., Mobarry C., Morris J., Moshreil A.,
RA Mulmi H., Kallsh F., Sandare S.D., C., Scheeler F., Shen H.,
RA Mang Z.-Y., Hassarman D.K., Sandaers R.D., C., Scheeler F., Shen H.,
RA Mang Z.-Y., Hassarman D.K., Sandaers R.D., C., Scheeler F., Shen H.,
RA Mill H., Sandaer R., Tector C., Turner R., Venter E., Mang A.H., Wang X.,
RA Mang Z.-Y., Wassarman D.A., Weinstock G.M., Weisenbach J.,
RA Mill H., Sandaer R., Chon S., Sandaer S.D., C.,
Ra Mang Z.-Y., Wassarman D.
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Best Local
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01-NOV-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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STRAIN-BERKELEY;
MEDLINE-20196006; PubMed-10731132;
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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                                   Newcastle
                                                                                                 Large protein.
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disease virus.
ssRNA negative-strand
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63.68;
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20,
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Last sequence update)
Last annotation updat
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Pred. No.
   viruses; Mononegavirales;
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                      084483;
01-NOV-1998
01-NOV-1998
01-DEC-2001
                                                                                                                                                                                                                                EMBL; AC07884
Hypothetical
SEQUENCE 13
                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
Hypothetical 14.5 kDa protein.
05JNBB0073N24.18.
0ryza sativa (Rice).
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                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
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Submitted (MAR-1999)
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SEQUENCE FROM N.A.
MEDLINE-20047980: PubMed=10580061;
MEDLINE-20047980: PubMed=10580061;
MeDatsion T., Buchholz U.J.,
                                                                         084483
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Methylated-DNA protein ADA OR CT477.
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NCBI_TaxID=11176;
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nes 7; Conserv
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|LSSFKAQE 10
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NCE 2204 AA; 248500 MW;
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Pro; IPR001016; Viral_RNA_pol_L.
                                                                                                                                                                                                                                al protein.
137 AA; 1
                      (TremBLrel. 08, Created)
(TremBLrel. 08, Last sequence update)
(TremBLrel. 19, Last annotation updat
                                                                                                                                                                                 Conservative
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                                                                        PRELIMINARY;
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87.5%;
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           cysteine
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           methyltransferase
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                     RA Azevedo V. Bertero M.G., Bessieres P., Bolotin A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Borriss R., Boursier L., Brans A., Errun M., Brignell S.C., Bron S.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Gilseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Leyine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Median N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rose M., Sadaie Y.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Setiguchi J., Sekowska A., Serror S.J., Serror P., Shin B.S., Soldo B.,
RA Takeuchi M., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Taseuchi M., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Viari A., Wanbutt R., Wedler E., Wedler H., Weitzeneder T.,
RA Viari A., Wanbutt R., Wedler E., Wedler H., Weitzeneder T.,
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O1-JAN-1998;
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Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind
Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE001321; AAC68077.1; InterPro; IPR001497; Methyltransf_1. Pfam; PF01035; Methyltransf_1; 1. PROSITE; PS00374; MGMT; UNKNOWN_1.
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
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           Tosato V., Uchiyama S., Viari A., Wambutt R., We
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70.08;
             Wedler E.,
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               Wedler H., Weitzenegger
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Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
Harmon G., The sequen
                          SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Harmon G., Wohldmann P.;
                                                                                                                             Science
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01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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SMART; SM0382; AAA; 1.
PROSTTE; PS00211; ABC_TRANSPORTER; 1.
ATP-binding; Transport; Complete proteome.
SEQUENCE 230 AA; 25272 MW; 59CDIFC50BD619DD CRC64;
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1. SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY (ABC TRANSPORTERS).

EMBL: Z99111; CAB13309.1; ...
EMBL: AF012285; AAC24910.1; ...
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003439; ABC_transportr.
Pfam: PF00005; ABC_tran; 1.
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Hemila H., Palva A., Paulin L., Arvidson S., Palva I "Secretory S complex of Bacillus subtilis: sequence identity to pyruvate dehydrogenase.";
J. Bacteriol. 172:5052-5063(1990).
                                                                                                                        "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                      None;
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Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
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sequence of C. elegans cosmid Y97E10B.";
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  BB
                       ITAM_MOUSE
RRPL_NDVB
NUOI_BUCAI
SP5K_BACSU
ASPG_HELPY
ASPG_HELPJ
YC44_ODOSI
                                                                                                                                                                                             HBB_GYMAC
UL79_HSV6U
ETFA_CAEEL
PAI1_PIG
ZF36_HUMAN
RA16_YEAST
LFC_CARRO
LFC_TACTR
                                                                                                                                                                                                                                                                                                                                                                                              TP2A_MOUSE
TP2A_HUMAN
TP2A_PIG
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VP16_HUMAN
VS14_TRYBB
RPN3_YEAST
YAG5_SCHPO
PA11_BOVIN
SBCC_LACLA
XN94_YEAST
LKHA_DICDI
RECE_AZOVI
RECE_AZOVI
TP2A_CRIGR
TP2A_CRIGR
TP2A_RAT
COPD_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
P40016
P13909
P13909
Q9Cfz0
Q9Cfz0
P539751
P529751
P4567
P41516
P41516
P41516
P41516
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P61388
P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P06734 homo sapien
075436 homo sapien
P26329 trypanosoma
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                    5 mus musculu
6 newcastle d
buchnera ap
8 bacillus su
14 helicobacte
9 helicobacte
9 odontella s
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7 mus musculu
8 homo sapien
4 sus scrofa
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mycoplasma
cricetulus
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2 dictyosteli
7 azotobacter
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bos taurus
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saccharomyc
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homo sapien
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1	TP2B_MOUSE	YJW2_YEAST	YIR3_YEAST	TOP2_CAEEL	BCC1_ACEXY	DIA3_MOUSE	RET_MOUSE	YAS5_SCHPO	TSCC_HUMAN	TSCC_RAT	DIA3_HUMAN	GIDA_RICPR
,	Q64511 mus musculu	_	w		P19450 acetobacter		P35546 mus musculu	Q10141 schizosacch				Q9ze90 rickettsia

ALIGNMENTS

RT RL	R A	RA	R R	R R	RT	Ŗ K	RA	Z ?	R	곱	R 7.7	RA S	RX	RP R	R RL	R. 7.	₽ ₽	RA	RA.	R X	RN	R.	2 Z	RA	RA	공 ※ 주	RN	2 2	38	SO	GN	문	DE :	Į Į	DŢ	ð:	RESULT FCE2_H
fic and IL-4-specific regulation of gene expr $618(1988)$.	"Two species of human Fc epsilon receptor II (Fc epsilon RII/CD23):	ķ	ALTERNATIVE SPLICING. MEDLINE-89028672; PubMed-2972386;	Biochem. J. 286:819-824(1992).		Jansen K.U., Magnenat E., Aubonney N., Bonneroy JY.; "Partial characterization of natural and recombinant human soluble	G., Graber P., Pochon S., Regamey	Med=1417742;		0 1.	expression of the cDNA c	Kilchherr E., Frost H., Delespesse G.;	87218454; PubMed=3034567;	SEQUENCE FROM N.A.	Cell 47:657-665(1986).	at structure of	Sakiyama F., Suemura M., Kishimoto T.;	Kaisho T., Uchibayashi N., Hardy R.R., Hir	S., Sato R., E	SEQUENCE FROM N.A. MEDLINE=87051737; PubMed=2877743;		Proc. Natl. Acad. Sci. U.S.A. 84:819-823(1987).	"Human Lymphocyte FC receptor for IgE: sequence nomology of its cloned cDNA with animal lectins.":	e T., Yodoi J.;	Ikuta K., Takami M., Kim C.W., Honjo T., Miyoshi T., Tagaya Y.,	SEQUENCE FROM N.A. MEDLINE=87118255: PubMed=2949326:		NCBI TRAXID=9606:	Chordata; Craniata; Vertebrata; E	sapiens (Human).	FCER2 OR IGEBF.	receptor) (FC-epsilon-RII) (CD23) (BLAST 2) (Immunoglobulin E-binding	n epsilon FC receptor (Lymphocyte	01-JAN-1988 (Ref. 06, Last sequence update)	1988 (Rel. 06, Creat		FORD HIMAN STANDARD: DRT

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35-STRUCTURE MODELING OF LECTIN DOMAIN.
MEDLINE-94191542; PubMed-8142907;
Padlan E.A., Helm B.A.;
"Modeling of the lectin-homology domains affinity Fc epsilon receptor (Fc epsilon Receptor 3:325-341(1993).
[7]
                                                                                                                                                                                                                                                                                                                                                                           EMBL; M15059; AAA52434.1; -.
EMBL; M14766; AAA52435.1; -.
EMBL; X04772; CAA28465.1; -.
EMBL; X04772; CAA28433.1; -.
PIR; A26067; LNHUER.
PIR; A26067; LNHUER.
PIR; A26589; A26589.
PIR; A31924; A31924.
PIR; J10132; J10132.
                                                                                                                                                                                     InterPro; IPKUULLU, Pfam; PF00059; lectin_C; l.
Pfam; PF00059; lectin_C; l.
SMART; SM00034; CLECT; l.
PROSITE; PS00615; C_TYPE_LECTIN_1; l.
PROSITE; PS50041; C_TYPE_LECTIN_2; l.
IqE-binding protein; Transmembrane; Glycoprotein; Receptor; B-cell; IqE-binding protein; Transmembrane; Glycoprotein; Receptor; B-cell; IqE-binding protein; Transmembrane; Glycoprotein; Receptor; B-cell; IqE-binding protein; Transmembrane; Alternative splicing; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bajorath J., Aruifo A.;

Bajorath J., Aruifo A.;

Structure-based modeling of the ligand binding domain of the human cell surface receptor CD23 and comparison of two independently derived molecular models.";

Protealn Sci. 5:240-247(1996).

1- FUNCTION: THIS RECEPTOR HAS ESSENTIAL ROLES IN THE REGULATION OF IGE PRODUCTION AND IN THE DIFFERENTIATION OF B-CELLS (IT IS A B-CELL-SPECIFIC ANTICEN).

1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS A SOLUBLE EXCRETED FORM.

A SOLUBLE EXCRETED FORM.

1- ALTERNATIVE PRODUCTS: 2 ISOPORMS; A (SHOWN HERE) AND B; ARE PRODUCED BY ALTERNATIVE SPLICING.
DISULFID
DISULFID
DISULFID
                                            DOMAIN
SITE
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstati the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entitles requires a license agreement (See http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                      PDB; 1HLI; 31-JAN-94.
PDB; 1KJE; 03-APR-96.
Genew; HGNC:3612; FCER2.
MIM; 151445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3D-STRUCTURE MODEL MEDLINE-96276216;
                                                                                                                       DOMAIN
                                                                                                                                                       TRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AND MONOCYTES.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
DATABASE: NAME-PROW; NOTE-CD guide CD23 entry;
WWW-"http://www.ncb1.nlm.nlh.gov/prow/cd/cd23.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTM: N- AND O-GLYCOSYLATED.
MISCELLANEOUS: THERE ARE TWO KINDS OF FC RECEPTORS FOR IGE, WHICH
DIFFER IN BOTH STRUCTURE AND FUNCTION: HIGH AFFINITY RECEPTORS ON
BASOPHILS AND MAST CELLS AND LOW AFFINITY RECEPTORS ON LYMPHOCYTES
 48
162
149
69
90
111
160
163
                                                                                                                                                    150
1
22
                                                                                                                                                ; Signal-anchor;
1 321 ME
0 321 SO
1 21 CY
2 47 SI
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 321
284
150
89
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131
288
174
                                                                                        EXTRACELLULAR (POTENTIAL)
C-TYPE LECTIN (LONG FORM)
CLEAVAGE.
                                                                                                                                                MEMBRANE BOUND FORM.
SOLUBLE FORM.
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE
              В
ХВ
                                                                                                                                     (POTENTIAL)
              SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (See http://www.isb-sib.ch/announce/
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VP26_HUMAN
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Best Local S
Matches 11
                           Matches
                                        Best
                                                   Query Match
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He K.-L., Gu B.-W., Han Z.-G., Shen
Wang Y.-X., Chen S.-J., Chen Z.;
"Identification of genes expressed i
stem/progenitor cells by expressed s
length CDNA cloning.";
Proc. Natl. Acad. Sci. U.S.A. 95:817
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CARBOHYD
VARSPLIC
CONFLICT
SEQUENCE
                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                          Renfrew Haft C., Sierra L., Bafford R., Barr V.A., Taylor S.I.; "Sorting nexins (SNX) 1 and 2: interaction domains involved in: association and associations with human retromer proteins."; Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                           Interpro; IPRO05377; Vps26.
Pfam; PF03643; Vps26; 1.
Transport; Protein transpor
SEQUENCE 327 AA; 38024 M
                                                                                                                                       EMBL; AF054179; AAC39912.1; -. EMBL; AF175266; AAF89954.1; -. Genew; HGNC:12711; VPS26.
                                                                                                                                                                                                                                                                                                                                           TISSUE=Colon;
Renfrew Haft C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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075436;
                                                                                                                              MIM; 605506;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-98318631; PubMed-9653160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Blood
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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16-OCT-2001 (Rel. 40, Last sequence u)
16-OCT-2001 (Rel. 40, Last annotation)
19526 protein homolog.
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                                       Local
 2 DLSSFKSQEL
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                          Similarity 7; Conserv
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321 AA;
                         Conservative
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Chordata;
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63
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38024 MW;
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                                                  Score 35;
                                                                                                                                                                                                                                                                                                                                                                                              95:8175-8180(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 51;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q.-H., Zhou
Shen Y., Gu
                                                                            BD330759ABE9BFA9 CRC64;
                           Mismatches
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Yu Y.-P.,
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                           Indels
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RESULT 3

VX14_TRYBB

VD VX14_TPYBB

VX14_TPYBB

VX14_TPYBB

VX14_TYBB

Q1 01-MAY

DT 01-MAY

RW 15-JUN

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DISULFID
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01-MAY-1992 (Rel. 22, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Variant surface 9lycoprotein ILTAT 1.24 precursor (VSG).
Trypanosoma brucel brucei.
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P26329;
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Pfam; PF00913; Trypan_glycop; 1.
Glycoprotein; Antigen; Trypanosomia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trypanosoma brucei.",
Nature 362:603-609(1993).

-i- FUNCTION: VSG FORMS A COAT ON THE SURFACE OF
TYPANOSOME EVADES THE IMMUNE RESPONSE OF THE
A SERIES OF ANTIGENICALLY DISTINCT VSGS FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-93218763; Publ
Blum M.L., Down J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-ISOlate MIAG 209;
MEDLINE-92046037; PubMed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; S18449; S18449
PDB; 2VSG; 25-NOV-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Turner M.J.
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                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                            PROPEP
                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                             3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X56767; CAA40086.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A structural motif in the variant surface glycoproteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wiley D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 24-381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Variant specific glycoprotein of Try domains each having an independently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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SDLNSFKTLEL 66
                                               ADLSSFKSQEL 11
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                                                                                         Similarity 7; Conser
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514
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                                                                                           Conservative
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ller N., Blum M.L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JATION: Attached to the membrane by a GPI-anchor IS RELASED FROM RUPTURED CELLS BY THE ACTION OF
                                                                                                                  68.6%;
63.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                   Trypanosomiasis; GPI-anchor; Membrane; Signal;
                                                                                                                                                                                       ¥,
                                                                                                               Score 35;
Pred. No.
                                                                                                                                                                                       GPI-ANCHOR (BY SIM)
E77395A9E9CFDC8E
                                                                                                                                                                                                           N-LINKED (GLCNAC. . .) (POTENTIAL) GPI-ANCHOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                       VARIANT SURFACE GLYCOPROTEIN ILTAT 1.24 HYDROPHOBIC, REMOVED DURING MATURATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                        Length 514;
                                                                                                                                                                                       CRC64;
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RESULT 4
RPN3_YEAST

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Matches
                       Query Match
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                                                                                                                                                                                                                                                                 This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kominami K.-I., Okura N., Kawamura M., Demartino G.N. Shimbara N., Chung C.H., Fujimuro M., Yokosawa H., Sanahashi N., Tanaka K., Toh-E A.; Tanahashi N., Tanaka K., Toh-E A.; "Yeast counterparts of subunits S5a and p58 (S3) of proteasome are encoded by two multicopy suppressors mol. Biol. Cell 8:171-187(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *Rawamura M., Kominami K.-I., Takeuchi J., Toh-E A.;

*A multicopy suppressor of nin1-1 of the yeast Saccharomyces
cerevisiae is a counterpart of the Drosophila melanogaster diphenol
oxidase A2 gene, Dox-A2.*;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1995 (Rel. 31, Created)
01-FEB-1996 (Rel. 33, Last sequence upo
15-JUN-2002 (Rel. 41, Last annotation upo
265 protessome regulatory subunit RPN3
                                                                                         SGD; S0000823; RPN3.
InterPro; IPR000717; PCI.
Pfam; PF01399; PCI; 1.
SMART; SM00088; PINT; 1.
                                                                                                                             EMBL; D78023; BAA11208.1;
EMBL; U18778; AAB64554.1;
SGD; S0000823; RPN3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=96242146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomycetales; Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P40016;
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                                                                 CONFLICT
                                                                              Proteasome
            Local
                                                                                                                                                                                                                                                                                                                                          PROTEINS.
SUBUNIT: THE 26S PROTEASOME IS COMPOSED OF A CORE PROTEASE,
AS THE 20S PROTEASOME, CAPPED AT ONE OR BOTH ENDS BY THE 19S
REGULATORY COMPLEX (RC). THE RC IS COMPOSED OF AT LEAST 18
DIFFERENT SUBUNITS IN TWO SUBCOMPLEXES, THE BASE AND THE LID
                                                                                                                                                                                                                         European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE PROTEASOME SUBUNIT S3 FAMILY.
                                                                                                                                                                                                                                                                                                      WHICH FORM THE PORTIONS PROXIMAL AND DISTAL CORE, RESPECTIVELY (BY SIMILARITY). DOMAIN: CONTAINS 1 PCI DOMAIN.
                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboration
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Similarity
7; Conser
                                                                                                                                                                                                                                                   the Swiss Institute of Bioinformatics
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60422
            68.6%;
70.0%;
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Last annotation updat
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Fujimuro M., Yokosawa H., Shimizu
                                                    Œ;
Pred. No. 16; 2; Mismatches
                      Score 35;
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                                                    -> G (IN REF. 3).
D0DA1645B8DE958D
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                        Length 523;
                                                     CRC64;
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nizu Y.,
                                                                                                                                                                                                                                                    EMBL outstation
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DLSSFKSQEL 11 |||| ::||| DLSSLRNQEL 68

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RESULT 5
YAQ5_SCHPO
                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                  REPEAT
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                                                                       EMBL; Z68198; CAA92385.1;
InterPro; IPRO00357; HEAT,
Pfam; PF02985; HEAT; 4.
PROSITE; PS50077; HEAT_RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Putative translational activator C18G6.05C (GCN1
SPAC18G6.05C.
                                                        Hypothetical
REPEAT :
                                                                                                                                                                                                                                                                                                                                                                                                                                              Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YAQ5_SCHPO
Q10105;
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                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces.
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   315
1062
1319
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1557
                                                                 protein;
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                                                    AT; 4.; HEAT_REPEAT; 4.; HEAT_REPEAT; 4.
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   HEAT
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on regulation; Activator; Repeat. AT 1.
AT 2.
AT 3.
AT 4.
AT 5.
AT 6.
AT 7.
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Best Local
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MEDLINE=90067867; PubMed=2587231;
Mimuro J., Sawdey M., Hatlori M., Loskutoff D.J.;
"CDNA for bovine type 1 plasminogen activator inh
Nucleic Acids Res. 17:8872-8872(1989).
[2]
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01-JAN-1990 (Rel. 13, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Plasminogen activator inhibitor 1 precursor (PAI-1) (Endothelial plasminogen activator inhibitor) (PAI).
SERPINE1 OR PAII.
                                                                                                                                                                                                                                                                                                                              MEDLINE-90338128; PubMed-1696269;
Pepper M.S., Belin D., Montesano R., Orci L., Vassalli J.-D.;
Pepper M.S., Belin D., Montesano R., Orci L., Vassalli J.-D.;
Pepper M.S., Belin D., Montesano R., Orci L., Vassalli J.-D.;
Proper M.S., Belin D., Montesano R., Orci L., Vassalli J.-D.;
Pepper M.S., Belin D., Montesano R., Orci L., Vassalli J.-D.;
Pepper M.S., Belin D., Montesano R., Orci L., Vassalli J.-D.;
Pepper M.S., Belin D., Montesano R., Orci L., Vassalli J.-D.;
Pepper M.S., Belin D., Montesano R., Orci L., Vassalli J.-D.;
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Pepper M.S., Belin D., Montesano R., Orci L., Vassalli J., Vassalli J.-D.;
Pepper M.S., Belin D., Montesano R., Orci L., Vassalli J., Vassalli J.-D.;
Pepper M.S., Belin D., Montesano R., Orci L., Vassalli J., Vassalli J.-D.;
Pepper M.S., Belin D., Montesano R., Orci L., Vassalli J., Vassalli J., Vassalli J.-D.;
Pepper M.S., Belin D., Vassalli J., 
                                            This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 24-63.
MEDLINE-88329072; PubMed-3262060;
Katagiri K., Okada K., Hattori H., Ya
"Bovine endothelial cell plasminogen
Purification and heat activation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BOVIN
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Bovidae; Bovinae; Bovidae; Bovidae; Bovidae; Bovinae; B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus (Bovine).
Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eur. J. Biochem. 176:81-87(1988).
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                                                                                                               FIBRINOLYSIS.
MISCELLANDOUS: PAI1 IS INACTIVATED BY PROTEOLYTIC ATTACK UROKINASE-TYPE (U-PA) AND THE TISSUE-TYPE (TPA), CLEAVING 369(R)-370(M) BOND.
MISCELLANDOUS: VASCULAR ENDOTHELIAL CELLS MAY BE THE PRIM OF SYNTHESIS OF PLASMA PAI.
SIMILARITY: BELONGS TO THE SERPIN FAMILY.
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Pred. No. 93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yano M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           activator inhibitor (PAI-1).";
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CONFLICT
SEQUENCE
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ACT_SITE
                                                                                                                                                                                            Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K., Weissenbach J., Ehrlich S.D., Sorokin A.;
Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lactococcus Lactis ssp. lactis II.1403.";
Genome Res. 11:731-753(2001).
-! FUNCTION: SbcCD Cleaves DNA hairpin structures. These structures can inhibit DNA replication and are intermediates in certain DNA recombination reactions. The complex acts as a 3'->5' double strand exonuclease that can open hairpin. It also has a 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-2002
15-JUN-2002
15-JUN-2002
                                         use by non-profit institutions as long as its content modified and this statement is not removed. Usage by arentities requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
                                                                                                           This SWISS-PROT entry is copyright. It is produced through a cheween the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                               Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                            Nuclease sbcCD subunit SBCC OR LL1321.
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Q9CFZ0;
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SMART; SM00093; SERPIN; 1.
PROSITE; PS00284; SERPIN; 1.
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PIR; S06745; S06745.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to_license@isb-sib.ch).
              EMBL; AE006364; AAK05419.1;
                                                                                                                                                                                                                                                                                                                          MEDLINE-21235186; PubMed-11337471;
                                                                                                                                                                                                                                                                                                                                             STRAIN-IL1403;
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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 InterPro; IPR003439;
                                                                                               the European Bioinformatics Institute.
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                                                                                                                                                    single-strand endonuclease activity (By similarity). SUBUNIT: Heterodimer of sbcC and sbcD (By similarity). SIMILARITY: BELONGS TO THE SMC FAMILY. SBCC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X16383; CAA34419.1; -. X52906; CAA37094.1; -.
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(Rel. 41, Last sequence update)
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REACTIVE BOND.
N-LINKED (GLCNAC. . .) (POTENTIAL).
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S -> L (IN REE. 2).
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Pred. No. 19;
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                                                     (See http://www.isb-sib.ch/announce/
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YN94_YEAST
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CARBOHYD
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DOMAIN
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Putative 125.2 kDa membrane glycoprotein in BIO3-HXT17 intergenic
                                              1056
                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                            Hilbert H., Moestl D.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE PEP1 FAMILY OF MEMBRANE GLYCOPROTEINS.
                                                                                                                                       SEQUENCE
                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                   CARBOHYD
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                                                                                                                                                                                                                               InterPro; IPR002860; GH_BNR. Pfam; PF02012; BNR; 7.
                                                                                                                                                                                                                                                      EMBL; Z71680; CAA96347.1; -. SGD; S0005348; YNR065C.
                                                                                                                                                                                                                                                                                       entities requires a license agreement (Some send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; I
Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
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P53751;
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                                                                                                                                                                                                                     Hypothetical
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                                              DLSSFTSQD 1064
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7; Conserv
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                                                                                                               Length 1116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomycetes
                                                                                                                                       CRC64;
                                                                                            Indels
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                                                                                                                                                           (POTENTIAL).
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(POTENTIAL).
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Best Local S
Matches 5
                                                                                                                                                                                                                                                       P49997;
01-OCT-1996
01-OCT-1996
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                          RECF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Leukotriene A-4 hydrolase (EC 3.3.2.6) (LTA-4 hydrolase) (Leukotriene
                                                                                                                                                                                                                         DNA replication
                                                                                                                                                                                                                                                                                                                                                                                                        RECF_AZOVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jho E., Kopachik W.;
Submitted (JUL-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
                                                                            Azotobacter
                                                                                                              Bacteria;
                                                                                                                                                Azotobacter vinelandii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01433; Pept1dase_ml; 1.
PROSITE; PS00142; ZINC_PROTEASE; PARTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001930; Ala_peptase.
InterPro; IPR000130; Zn_MTpeptdse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEROPS; M01.004; -.
DictyDb; DD05072; lkha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U27538; AAA70101.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A(4) hydrolase) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Metalloprotease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Multifunctional enzyme; Hydrolase; Leukotriene biosynthesis; Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               196
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CATALYTIC ACTIVITY: (7E,9E,112,142)-(5S,6S)-5,6-epoxyicosa-7,9,11.14-tetraenoate + H(2)O = (6Z,8E,10E,14Z)-(5S,12R)-5,12-dihydroxyicosa-6,8,10,14-tetraenoate.

COPACTOR: BINDS 1 ZINC ION (BY SIMILARITY).

PATHWAY: Leukottienes biosynthesis; third step.

SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

SIMILARITY: BELONGS TO PEPTIDASE FAMILY M1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
FUNCTION: Hydrolyzes an epoxide moiety of leukotriene A4 (LTA-4)
to form leukotriene B4 (LTB-4). The enzyme also has some peptida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIKSFKTQQI 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DLSSFKSQEL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the Swiss Institute of Bioinformatics
                                                                                                          Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2
4
23
90
316
                                                                                                                                                                                                         (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 41, Last annotation updat
tion and repair protein recF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Α
                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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36594
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                                                                                                          gamma
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
PROTON DONOR (POTENTIAL).
E8307415B991487A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                          subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                            364
                                                                                                                                                                                                                                                       update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and the EMBL outstation
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GGT_PSESP

GGT_PSESP

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AC P3626

DT 01-JU

DT 01-WO

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DT GAMMA

GN GGT...

OS Pseud

OC Bacte

OX NCBI_RN [1]

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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                GGT_PSESP
P36267;
            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                             Ishiye M., Yamashita M., Niwa "Molecular cloning of the gamm Pseudomonas strain.";
                                                                                                                                                                                                                                                                               01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-WOV-1997 (Rel. 35, Last annotation update)
Gamma-glutamyltranspeptidase precursor (EC 2.3.2.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X86404; CAA60158.1; -.
InterPro; IPR001238; RecF.
InterPro; IPR003395; SMC_N.
Pfam; PF02463; SMC_N; 1.
                                                                                                                           Pseudomonas strain.
                                                                                                                                                                     MEDLINE=93305254; PubMed=7765305
                                                                                                                                                                                       SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                     Pseudomonas sp. (strain Al4).
Bacteria; Proteobacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00617; RECF_1; 1. PROSITE; PS00618; RECF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGRFAMS; TIGRO0611; recf; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene 162:47-51(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-96009876; PubMed-7557415; Badran H., Venkatesh T.V., Kunnim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-UW;
                                                                                                                                                                                                                    NCBI_TaxID=306;
                                                                                                                                                                                                                                                                                                                                 01-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA damage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Badran H., Venkatesh T.V., Kunnimalaiyaan M., Sharma N., Das H.K., ^{*}Molecular characterization of the Azotobacter vinelandii recF gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                           64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TO BIND ATP.
SUBCELLULAR LOCATION: Cytoplasmic (Potential).
SIMILARITY: BELONGS TO THE RECF FAMILY.
CAUTION: This entry seems to be produced by an incorrect sequence that contains at least 14 frameshifts. Do not use it for any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: THE RECF PROTEIN IS INVOLVED IN DNA METABOLISM; IT IS REQUIRED FOR DNA REPLICATION AND NORMAL SOS INDUCIBILITY. RECF BINDS PREFERENTIALLY TO SINGLE-STRANDED, LINEAR DNA. IT ALSO SEEMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                phylogenetic purpose.
                                                                                                                                                                                                                                                                                                                                                                                                                                        LSSFRSQRL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSSFKSQEL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     364 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA replication; DNA-binding; SOS response; DNA repair;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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244
                                                                                                                                                                                         AND PARTIAL
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77.88;
                                                                                                                                        gamma-glutamyltranspeptidase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 33;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARG-RICH (BASIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP (POTENTIAL).
                                                                                                                                                          3
                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BFF65FDB63AC8407 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                  575
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                                                                                                                                          gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein MPN364 (H91_orf677).
MPN364 OR MP472.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YD64_MYCPN
P75417;
16-OCT-2001
16-OCT-2001
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000101; Gglutrnspptdase Pfam; PF01019; G_glu_transpept; 1. PRINTS; PR01210; GGTRANSPTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (So or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
     Pfam; PF03202; Lipoprotein_10;
Pfam; PF03305; Lipoprotein_x;
Hypothetical protein; Complete
SEQUENCE 677 AA; 75591 MW;
                                                                                                                                                                                                  modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    pneumoniae."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; PubMed-8948633;
Himmelreich R., Hilbert H., Plage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycoplasma pneumoniae 
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glutathione biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGRFAMS; TIGR00066; g_glut_trans; 1. PROSITE; PS00462; G_GLU_TRANSPEPTIDASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEROPS; T03.001;
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                                                                                              InterPro; IPR004890; Lipoprotein_10.
InterPro; IPR004984; Lipoprotein_X.
                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=2104;
                                                                                                                                                      EMBL; AE000047; AAB96120.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete sequence analysis of the genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Herrmann R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     251 ADLDQYKTREL
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                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS
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                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collable the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions
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6; Conserv
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377
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575 AA;
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376
575
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450
61301 MW;
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LONGS TO THE MG185 / MG260 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54.78;
                            Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plagens H., Pirkl E., Li B.-C.
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Pred. No.
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     proteome.
E785B68BD679F04D CRC64;
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RESULT 13
TP2A_CRIGR
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Best Local
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P41515;
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation updat
DNA topoisomerase II, alpha isozyme (EC 5.9
TOP2A OR TOP2 OR TOP-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OVATY cell line.";
J. Biol. Chem. 268:2160-2165(1993).
J. FUNCTION: CONTROL OF TOPOLOGICAL S
BREAKAGE AND SUBSEQUENT REJOINING
MAKES DOUBLE-STRAND BREAKS.
-!- CATALYTIC ACTIVITY: ATP-dependent
                                          NP_BIND
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cricetulus griseus (Chinese hamster).
Eukaryota; Metazoa; Chordata; Craniat
                                                                                              PRINTS: PRO0615; CCAATSUBUNTA.
PRINTS: PRO0418; TP12FAMILY.
ProDom: PD000616; DNA_topoisoIV;
ProDom: PD000742; DNA_topoisoIV;
SMART; SM00433; TOP2c; 1.
SMART; SM00434; TOP4c; 1.
                                                                                                                                                                                 InterPro; IPR003957; CBFA_NFYB_topis.
InterPro; IPR001241; DNA_topoisoII.
InterPro; IPR002205; DNA_topoisoIV.
Pfam; PF00204; DNA_gyraseB; 1.
Pfam; PF00521; DNA_topoisoIV; 1.
Pfam; PF00518; HATPase_C; 1.
                                                                                                                                                                                                                                                                                   EMBL; L04607; AAA37023.1; -. HSSP; P06786; 1BGW.
                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                      This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chan V.T., Ng S.W., Eder J.P., Schnipper L.E.; "Molecular cloning and identification of a point mutation topoisomerase II cDNA from an etoposide resistant Chinese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular cloning and identification
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                         the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                    PROSITE;
                                                                                                                                                                                                                                                                       InterPro; IPR003594; ATPbind_ATPase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: HOMODIMER.
SUBCELLULAR LOCATION: Nuclear.
SUBCELLULAR LOCATION: TOPOISOMERASE I
                                                                                                                                                                                                                                                                                                                                                                                                                                            MISCELLANDOUS: EUKARYOTIC TOPOISOMERASE I AND II CAN RELA
NEGATIVE AND POSITIVE SUPERCOILS, WHEREAS PROKARYOTIC EN:
RELAX ONLY NEGATIVE SUPERCOILS.
SIMILARITY: BELONGS TO THE TYPE II TOPOISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                         European Bioinformatics Institute. There are no rest by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of double-stranded DNA.
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                            Topoisomerase; 1
160 165
804 804
493 493
 1526
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A,
        TOPOISOMERASE_II; 1.

TOPOISOMERASE_II; 1.

OMETASE; DNA-binding; ATP-binding; Nuclear protein.

165 ATP (POTENTIAL).

804 DNA CLEAVAGE (BY SIMILARITY).

804 R -> Q (IN CELLS RESISTANT TO THE

493 R -> Q (IN CELLS RESISTANT TO THE

ANTINEOPLASTIC AGENTS VP-16 AND VM-26).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64.7%;
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Pred. No.
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ENZYMES
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Best Local S
Matches 7
                                                                                                                        PRINTS: PRO0615; CCAATSUBUNTA.
PRINTS: PRO0418; TPT2FAMILY.
PRODOM: PD000616; DNA_topoisoI; 1
ProDom: PD000742; DNA_topoisoIV; 1
SMART; SM00433; TOP2C; 1.
SMART; SM00434; TOP4C; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-Sprague-Dawley: TISSUE-Testis; MEDLINE-93390677; PubMed-8390253; Park S.H., Yoon J.H., Kwon Y.D., Park S.D. "Nucleotide sequence analysis of the CDNA II.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                     InterPro;
InterPro;
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Mammalia; Eutheria;
NCBI_TaxID=10116;
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                                                                                                         PROSITE;
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FUNCTION: CONTROL OF TOPOLOGICAL STATES OF I
BREAKAGE AND SUBSEQUENT REJOINING OF DNA STE
MAKES DOUBLE-STRAND BREAKS.
CATALYTIC ACTIVITY: ATP-dependent breakage,
of double-stranded DNA.
SUBUNIT: HOMODIMER.
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SIMILARITY: BELONGS TO THE TYPE II TOPOISOMERASE FAMILY.
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PF00521; DNA_topo1soIV; 1.
PF02518; HATPase___; 1.
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P06786;
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PS00177; TOPOISOMERASE_II; 1.

1e; Topoisomerase; DNA-binding; Nucle
159 164 ATP (POTENTIAL).

159 803 B03 DNA CLEAVAGE (BY SIMILARITY)

1526 AA; 173220 MW; A1961ABBDB1B050F CRC64;
                                                                                                                                                                                                                                                                                                                                                  IPR003594; ATPbind_ATPase.
IPR003957; CBFA_NFYB_topis.
IPR001241; DNA_topoisoII.
IPR002205; DNA_topoisoIV.
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70.0%;
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OF TOPOLOGICAL STATES OF DNA BY
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Pred.
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Sciurognathi; Muridae;
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01-APR-1993
01-APR-1993
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                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-94084643; PubMed-8261398;
MCPherson J., Brown G.A., Goldenberg G.J.;
"Characterization of a DNA topoisomerase IIalpha gene rearrangement in adriamycin-resistant p388 leukemia: expression of a fusion messenger RNA transcript encoding topoisomerase IIalpha and the retinoic acid receptor alpha locus.";
Cancer Res. 53:5885-5889(1993).
-I- FUNCTION: CONTROL OF TOPOLOGICAL STATES OF DNA BY TRANSIENT BREAKAGE AND SUBSEQUENT REJOINING OF DNA STRANDS. TOPOISOMERASE
                                                                                                  EMBL; D12513; BAA02076.1; -.
EMBL; U01915; AAC55135.1; -.
PIR; JS0703; JS0703.
PIR; S35483; S35483.
HSSP; P06786; 1BGW.
                                                                                                                                                                          between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as i modified and this statement is not removed. Use entitles requires a license agreement (See http or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=93065194; PubMed=1331984;
Adachi N., Miyaike M., Ikeda H., Kikuchi A.;
"Characterization of cDNA encoding the mouse
that can complement the budding yeast top2 mu
Nucleic Acids Res. 20:5297-5303(1992).
[2]
                                                                                        MGD;
                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration -
                                                                                                                                                                                                                                                                                -i- MISCELLANEOUS: EUKARYOTIC TOPOLSOMERASE I AND II CAN REL
NEGATIVE AND POSITIVE SUPERCOILS, WHEREAS PROKARYOTIC EN
RELAX ONLY NEGATIVE SUPERCOILS.
-i- SIMILARITY: BELONGS TO THE TYPE II TOPOISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                  MAKES DOUBLE-STRAND BREAKS.
-!- CATALYTIC ACTIVITY: ATP-dependent breakage,
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Mammalia; Eutheria;
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                                                                         InterPro;
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                                  MGI:98790; Top2a.

RPTO; IPR003594; ATPbind_ATPase.

RPTO; IPR003957; CBFA_NFYB_topis

RPTO; IPR001241; DNA_topoisoII.

RPTO; IPR002205; DNA_topoisoIV.
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                        PF00204;
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zeta-carotene desa	S43324	N	499	62.7	32	45
probable splicing	E84745	N	475	62.7	32	44
kynurenine-oxoglut	S66270	N	457	62.7	32	3
hypothetical prote	T20403	N	393	62.7	32	42
hypothetical prote	A71146	N	385	62.7	32	41
	T48341	N	337	62.7	32	40
hypothetical prote	T21451	N	316	62.7	32	39
protein F27D4.1 (i	D87839	N	316	62.7	32	38
hypothetical prote	F96758	N	312	62.7	32	37
ubiquinol-cytochro	T48591	N	274	62.7	32	36
hypothetical prote	T44199	N	258	62.7	32	35
probable hemeolysi	C81406	N	253	62.7	32	34
hypothetical prote	T44012	N	199	62.7	32	ω ω
hemoglobin beta ch	S20271	2	146	62.7	32	32
troponin I alpha -	JC5611	N	142	62.7	3 2	31
DNA topoisomerase	A40493	2	1530	64.7	u u	30

ALIGNMENTS

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A;Molecule type: mRNA
A;Rosidues: 1-268'T',270-321 <LUD>
A;Rosidues: 1-268'T',270-321 <LUD>
A;Cross-references: GE:X04772; NID:g34002; PIDN:CAA28465.1; PID:g34003
A;Cross-references: GE:X04772; NID:g34003
A;Cross-references: GE:X04772; NID:g34002; PIDN:GAA28465.1; PID:g34003
A;Cross-references: GE:X04772; NID:g34003
A;Cross-references: GE:X04772; NID:g34002; PIDN:GAA28465.1; PID:g34003
A;Cross-references: GE:X04772; NID:g34003
A;Cross-references: GE:X04772; NI

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submitted to the Brookhaven Protein Data Bank, November 1995

A;Reference number: A65963; PDB:IKIE

A;Contents: annotation; conformation by theoretical model, residues 173-285

C;Comment: The sequence of the splice form a is shown.

C;Comment: This receptor for the Fc portion of IgE is expressed in various hematopoietic elis.

C;Comment: Splice form a is expressed constitutively in B-cells; b is expressed in other C;Comment: Soluble IgE-binding factors are produced by proteolytic cleavage of IgE Fc re C;Comment: Soluble IgE-binding factors are produced by proteolytic cleavage of IgE Fc re C;Genetics:

A;Gene: GDB:FCER2; FCE2

A;Cross-references: GDB:I18888; OMIM:151445

A;Introns: B/1; 46/1; 64/1; 85/1; 106/1; 127/1; 157/1; 207/3; 243/2

C;Superfamily: IgE receptor II; C-type lectin homology

C;Keywords: alternative splicing; B-cell; glycoprotein; immunoglobulin receptor; macroph F; MNPPSQD', 47-321/Product: IgE Fc receptor II, splice form b *status predicted <SFBI>F;1-321/Product: IgE Fc receptor II, splice form b *status predicted <SFBI>F;1-321/Product: IgE Fc receptor II, splice form b *status predicted <SFBI>F;1-7,'b',47-321/Product: IgE Fc receptor II, splice form b *status predicted <SFBI>F;1-7,'b',47-321/Product: IgE Fc receptor II, splice form b *status predicted <SFBI>F;1-7,'b',47-321/Product: IgE Fc receptor II, splice form b *status predicted <SFBI>F;1-7,'b',47-321/Product: IgE Fc receptor II, splice form b *status predicted <SFBI>F;1-7,'b',47-321/Product: IgE Fc receptor II, splice form b *status predicted <SFBI>Files Fc receptor II, splice form b *status predicted <SFBI>Files Fc receptor II, splice form b *status predicted <SFBI>Files Fc receptor II, splice form b *status predicted <SFBI>Files Fc receptor II, splice form b *status predicted <SFBI>Files Fc receptor II, splice form b *status predicted <SFBI>Files Fc receptor II, splice form b *status predicted <SFBI>Files Fc receptor II, splice form b *status predicted <SFBI>Files Fc receptor II, splice form b *status predicted <SFBI>Files Fc recepto
                                                                                  F;1-7, D, 47-321/Product: IGE FG receptor II. splice form a' #status predicted < F;14-20/Region: stop-transfer sequence F;24-45/Domain: ctransmembrane #status predicted <TMM> F;46-321/Domain: ctracellular #status predicted <EXT> F;64-84/Region: 21-residue repeat F;81-321/Product: soluble IgE-binding factor (37K) #status predicted <IGE> F;81-321/Product: soluble IgE-binding factor (38K) #status predicted <IGE> F;102-321/Product: soluble IgE-binding factor (29K) #status predicted <IGE> F;106-126/Region: 21-residue repeat F;102-321/Product: soluble IgE-binding factor (25-27K), long form #status experi F;148-321/Product: soluble IgE-binding factor (25-27K), short form #status experi F;163-282/Domain: C-type lectin homology <LCH> F;163-282/Domain: C-type lectin homology <LCH> F;167-148/Cleavage site: Lys-Leu (unidentified proteinase) #status experimental F;147-148/Cleavage site: Arg-Met (unidentified proteinase) #status experimental F;191-282,259-273/Disulfide bonds: #status experimental
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A; Residues: 'MNPPSO', B-14 <YOK>
A; Residues: 'MNPPSO', B-14 <YOK>
A; Residues: 'MNPPSO', B-14 <YOK>
A; Cross-references: GB:M23562; NID:g182444
A; Experimental source: splice form IIb
A; Experimental source: splice form IIb
R; Lettellier, M.; Sarfati, M.; Delespesse, G.
Mol. Immunol. 26, 1105-1112; M99
A; Title: Mechanisms of formation of IgE-binding factors (soluble CD23)-I. Fc epsilon: A; Reference number: JL0132; MUID:90220658; PMID:2534424
A; Accession: JL0132
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A:Title: Partial characterization of natural and recombinant human soluble CD23 A:Reference number: S29107; MUID:93038513; PMID:1417742
A;Accession: S29107
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A;Note: part of this sequence, including the amino end of soluble forms of the protein, A;Note: A,;Kitutani, H.; Tanaka, T.; Sato, R.; Barsumian, E.L.; Suemura, M.; Kishimot Cell 55, 611-618, 1988
A;Title: Two species of human Fc-epsilon receptor II (Fc-epsilon-RII/CD23): tissue-speci A;Reference number: A31924; MUID:89028672; PMID:2972386
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submitted to the Brookhaven Protein Data Bank, June 1993
A;Reference number: A51791; PDB:1HLI
A;Contents: annotation; conformation by theoretical model, residues 173-285
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A; Accession: A26589
A; Molecule type: mRNA
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A; Residues: 152-166;173-179;189-212;230-263;268-306
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A; Dealus France, DNA
A; Molecule type; DNA
A; Residues: 1-4131 <WIL>
A; Cross-references: EMBL: Z75536; PIDN: CAA99830.1; GSPDB: GN00019; CESP: F18C12.1
A: Fynerimental source: clone F18C12
                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein F18C12.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 *sequence_revision 15-Oct-1999 *text_change 17-Mar-2000 C;Accession: T21085 R;Harris, B.
                                                                      A;Map position: 1
A;Introns: 54/3; 112/3; 146/1; 294/1; 381/3; 455/3; 596/3; 716/3; 743/2; 782/3; 820/3
A;Introns: 54/3; 112/3; 146/1; 294/1; 381/3; 455/3; 596/3; 716/3; 743/2; 782/3; 09/3; 2303/3; 2483/1; 2529/1; 2612/3; 2687/1; 2734/3; 2799/3; 2841/3; 2891/2; 2932/3;
C;Superfamily: dynein heavy chain, cytosolic
                                                                                                                                                                                                                                                                                                                     A; Reference number: A; Accession: T21085
                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, June 1996 A; Reference number: {\tt Z19371}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-305 <WI2>
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A;EXperimental source: clone F39H2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-305 <W
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A; Accession: T22009
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C;Accession: T22009; T23398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein F39H2.3 - Caenorhabditis elegans C; Species: Caenorhabditis elegans
                                                                                                                                                                     A; Gene: CESP:F18C12.1
                                                                                                                                                                                                                                                                                                 A; Status: preliminary; translated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, October 1996
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                   Query Match
Best Local
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Similarity
8; Conserv
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8; Conserv
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2
                   Score 37; Pred. No.
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Pred. No.
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1; Mismatches
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ADLSSFKSQEL 11

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R;Carrington, M.; Miller, N.; Blum, M.; Roditi, I.; Wiley, D.; Turner, M. J. Mol. Biol. 221, 823-835, 1991
A;Title: Variant specific glycoprotein of Trypanosoma brucei consists of A;Reference number: S18445; MUID:92046037; PMID:1942032
A;Accession: S18449
                                                                                                                                                                                                                                                                        RESULT 6
S18449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-glycoprotein E - Leishmania tropica
C;Species: Leishmania tropica
C;Species: Leishmania tropica
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
C;Accession: T18344
R;Lafuente, E.; Castanys, S.; Gamarro, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phosphotransacetylase UU066 [imported] - Ureaplasma urealyticum C;Species: Ureaplasma urealyticum C;Species: Ureaplasma urealyticum C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 C;Accession: C82938 R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, submitted to GenBank, February 2000 A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views
A; Molecule type: mRNA
A; Residues: 1-514 <CAR>
A; Cross-references: EMBL: X56767; NID: g10453; PIDN: CAA40086.1; PID: g10454
C; Superfamily: variant surface glycoprotein
                                                                                                                                                                                         variant surface glycoprotein ILTat 1.24 - Trypanosoma brucei
C;SpecLes: Trypanosoma brucei
C;Date: 16-Sep-1992 *sequence_revision 16-Sep-1992 *text_change 20-Aug-1999
C;Accession: S18449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-1677 <LAF>
A;Cross-references: EMBL:U55381; NID:g1916605; PID:g1916606; PIDN:AAB51191.1
C;Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology
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A; Accession: C82938
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A; Accession: T18344
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A;Genetic code: SGC3
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A; Residues: 1-293 <GLA>
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Pred. No.
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RESULT 8
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S50479
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                                                                                                                                                                                                                                                                                                                                  GCN1 homolog - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 07-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position:
C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: SGD:RPN3; SUN2; MIPS:YER021w
A;Cross-references: SGD:S0000823; MIPS:YER021w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: S50433
A; Accession: S50479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, December A;Description: The sequence of S. cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Saccharomyces cerevisiae
C;Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 23-Mar-2001
C;Accession: S50479
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Best Local Similarity
7; Conserve
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A; Accession: T37919
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A; Map position: 5R
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A; Residues: 1-523 <DIE>
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                                                                                                                      A; Introns: 50/1
                                                                                                                                                                   C; Genetics:
                                                                                                                                                                                 A; Experimental source:
                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-2670 < CON>
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                                                                                                                                     A; Map position:
                                                                                                                                                     A; Gene:
                                                                                                                                                                                                 A; Cross-references:
                                                                                                                                                                                                                                            A; Status:
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                                                                                                                                                                                                                                          preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                               DLSSLRNQEL 68
ADTSNFSNQEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 7; Conserv
                                                          Similarity 7; Conserv
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 682
                                                                                                                                                                                 strain
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                                                                                                                                                                                98; PIDN:CAA92385.1; 972h-; cosmid c18G6
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Pred. No.
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Pred. No.
                                                                        Score 35;
Pred. No.
                                                            Mismatches
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43;
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44;
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cosmids
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2.4e+02;
2;
                                                                                          DВ
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                                                            Indels
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Chlamydia trachomatis (serotype

D, strain UW3/Cx)

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C;Accession: B71510
R;Stephens, R.S.; Kalman, S.;
Science 282, 754-759, 1998
A;Title: Genome sequence of at
A;Reference number: A71570; M
A;Accession: B71510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cha A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

N;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler Iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Konlogstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueelly, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiquchi, J.; Sekowska, A.; Serotekuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchlyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yashikawa, H.; Danchin, A.; Reference number: A69580; MUID:98044033; PMID:9384377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accessiu. .....
A;Status; preliminary
A;Molecule type: DNA
A;Residues: 1-170 <ARN>
A;Cross-references: GB:AE001321; GB:AE001273; NID:g3328906; PIDN:AAC68077.1; PID:g332891
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                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: short-chain ATP-binding cassette proteins;
C;Keywords: ATP; nucleotide binding; P-loop
F;21-216/Domain: ATP-binding cassette homology <ABC>
F;38-45/Region: nucleotide-binding motif A (P-loop)
  hypothetical protein F31E8.6 - Caenorhabditis elegans C; Species: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:Z99111; GB:AL009126; NID:g2633699; PIDN:CAB13309.1; A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-230 <KUN>
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C;Species: Bacillus subtills
C;Date: 05-Dec-1997 #sequence_revision
C;Accession: D69858
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C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
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nes 6; Conserv
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7; Conserv
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60.0%;
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70.0%;
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                                                                                                                                                                                                                                                                                     Score 34;
Pred. No.
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Pred. No.
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A:Molecule type: protein
A:Residues: 24-49; L; 51-63 <KAT>
C:Comment: Three types of PAI have been identified. PAI-1
may be the primary site of synthesis of plasma PAI.
C:Comment: This inhibitor acts as "bait" for tissue plasmi
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 153-235 PEP>
A;Residues: 153-235 CPEP>
A;Cross references: EMBL:X52906; NID:g598; PIDN:CAA37094.1; PID:g930005
A;Cross references: EMBL:X52906; NID:g598; PIDN:CAA37094.1; PID:g930005
R;Katagiri, K.; Okada, K.; Hattori, H.; Yano, M.
Eur. J. Biochem. 176, 81-87, 1988
Eur. J. Biochem. 176, 81-87, 1988
A;Title: Bovine endothelial cell plasminogen activator inhibitor. Purification and A;Reference number: S01324; MUID:88329072; PMID:3262060
A;Accession: S01324
A;Accession: S01324
                                                                                                 C:Keywords: glycoprotein; serine proteinase inhibitor
F:11-25/Domain: signal sequence #status predicted <SIG>
F:24-402/Product: plasminogen activator inhibitor 1 #status predicted <MAT>
F:232,288,352/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:369/Inhibitory site: Arg (plasminogen activator) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X16383; NID:9600; PIDN:CAA34419.1; P. R;Pepper, M.S.; Belin, D.; Montesano, R.; Orci, L.; Vassalli, J. Cell Biol. 111, 743-755, 1990
A;Title: Transforming growth factor-beta 1 modulates basic fil A;Reference number: A35855; MUID:90338128; PMID:1696269
A;Accession: A35855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 plasminogen activator inhibitor-1 precursor - bovine
%;Alternate names: endothelial-cell plasminogen activator inhibitor; PAI-1
C;Species: Bos primigenius taurus (cattle)
C;Date: 28-Feb-1990 #sequence_revision 22-Apr-1995 #text_change 18-Jun-1995
C;Accession: S06745; A35855; S01324; S10906
R;Mimuro, J.; Sawdey, M.; Hattori, M.; Luskutoff, D.J.
Nucleic Acids Res. 17, 8872, 1989
A;Title: cDNA for bovine type 1 plasminogen activator inhibitor (PAI-1).
A;Reference number: S06745; MUID:90067867; PMID:2587231
                                                                                                                                                                                                                                        C; Comment: Glycosylation is not a prerequisite for C; Superfamily: antithrombin III
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S06745
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A; Residues: 1-402 <MIM>
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A; Residues: 1-270 < DUZ>
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C;Accession: T16227
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  Similarity
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                           66.78;
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70.0%;
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                         Score 34;
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submitted to the Protein Sequence Database, April 1996
A;Reference number: S62944
A;Reference number: S62944
A;Recession: S63397
A;Molecule type: DNA
A;Residues: 1-1116 <DUE>
A;Cross-references: EMBL:Z71680; NID:g1302593; PID:e239847; PID:g1302594; GSPDB:GN00014;
A;Experimental source: Strain S288C
C;GenetLcs:
A;Gene: MIPS:YNR055C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis sea, Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: A86790
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP-dependent dsDNA exonuclease [imported] - Lactococcus lactis subsp. lactis (strain C;Species: Lactococcus lactis subsp. lactis C;Species: Lactococcus lactis subsp. lactis (c;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: SGD:S0005348
A;Map position: 14R
C;Keywords: transmembrane protein
F;941-957/Domain: transmembrane #status predicted <TM1>
F;990-1006/Domain: transmembrane #status predicted <TM2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable membrane protein YNR065c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein N3539
C;Species: Saccharomyces cerevisiae
C;Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 19-Apr-2002
C;Accession: S63397
R;Duesterhoeft, A.; Floeth, M.; Fritz, C.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D. submitted to the Protein Sequence Database, April 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA A; Rostidues: 1-1046 <STO>
A; Restidues: 1-1046 <STO>
A; Cross-references: GB:AE005176; PID:g12724301; PIDN:AAK05419.1; GSPDB:GN00146
A; Experimental source: strain IL1403
C; Genetics:
A; Gene: sbcC
                                                                                      hypothetical protein HP0256 - Helicobacter pylori (strain 26695)
C;Spectes: Helicobacter pylori
C;Date: 09-Aug-1997 *sequence_revision 09-Aug-1997 *text_change 08-Oct-1999
C;Accession: H64551
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R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenneson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
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Pred. No. 1.5e+0
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Pred. No. 1.4e+02;
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Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: H64551
Search completed: March 13, 2003, 18:52:57 Job time: 12.8 secs
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                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-142 <TOM>
                                                                                                                                                                                                                                                                              A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                           A;Cross-references: GB:AE000545; GB:AE000511; NID:g2313349; PIDN:AAD07334.1; PID:g23
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                                                                                                                                                                    64.7%;
63.6%;
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pred. No. 29;
2; Mismatches
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Maximum DB seq length: 2000000000
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                             Length DB
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AAP82073
AAP81163
AAP81230
AAP81172
AAP81172
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50.197 Million cell updates/sec
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             Human soluble CD23
Human soluble CD23
Sequence containin
IgE binding factor
Recombinant Fc_eps
Low affinity Fc_ep
Fc gamma receptor.
Human IgE binding
Sequence encoded b
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AAP82839 AAB85396 AAW55865 AAW55494 AAW41679 ABB66544 AAB66524 AAB66524 AAB66524 AAB66524 AAB66544 AAB653465 AAW11459 AAB65465 AAU14597 AAB656747 AAB656747 AAB656747 AAB656747 AAB656747 AAB656747 AAB656747 AAB656747 AAB65677 AAB65677 AAB65677 AAG59808	AAP90367 AAR42053 AAW13142
X 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Peptide sequence o IgE binding factor Sequence containin

ALIGNMENTS

AAW13146 RESULT 1

AAW13146 standard; Protein; 166 AA

Human soluble CD23 isoform D.

17-JUN-1997 AAW13146;

(first entry)

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(LYNC/) LYNCH R G. (MATS/) MATSUI M. (NUNE/) NUNEZ R M. (YODO/) YODOI J.
DNA sequence encoding a soluble isoform scale preparation of the protein
                       WPI; 1997-159094/15.
N-PSDB; AAT61959.
                                                                                   28-DEC-1994;
                                                                                                 27-DEC-1995;
                                                                                                                 04-FEB-1997.
                                                                                                                               JP09028385-A.
                                                                                                                                              Homo sapiens
                                                                                                                                                           Human; soluble; CD23; complementarity determining; isoform D; recombinant production.
                                                                                  94US-0365103
                                                                                                 95JP-0341169
         of CD23 -
         useful for large
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AAP90120

Human lymphocyte

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RESULT 2
AAW13148
ID AW1
XX AAW1
AC AAW1
XX AW1
XX Huma
XX Huma
XX Huma
XX Huma
XX Homc
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Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (LYNC/) LYNCH R G. (MATS/) MATSUI M. (NUNE/) NUNEZ R M. (YODO/) YODOI J.
                                                                                                                                                                                                                                                                                         The cDNA encoding the present sequence, human soluble CD23 isoform C, can be used for the large scale recombinant proof soluble CD23.
                                                                                                                                             Sequence
                                                                                                                                                                                        The specification states that the nucleotide sequences contained in figures 4a-b, 5a-b, 12a-12b and 13a-b are claimed, however thouse scheme does not relate to the scheme used in the relevance of the specification.
                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Figure 15; 33pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA sequence encoding a soluble isoform scale preparation of the protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-159094/15.
N-PSDB; AAT61961.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human soluble CD23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW13148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The cDNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     isoform
                                          / Match 100.0%;
Local Similarity 100.0%;
hes 11; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79 ADLSSFKSQEL 89
  \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADLSSFKSQEL 11
  ADLSSFKSQEL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Figure 16; 33pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ncoding the present sequence, human soluble CD23 can be used for the large scale recombinant pro-
                                                                                                                                             167 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94US-0365103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95JP-0341169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ņ
                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 51;
Pred. No.
                                                                   Score 51; DB 18
Pred. No. 0.058;
                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               of CD23 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
                                                                                            18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18;
                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                            Length 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 166;
                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful for large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                in the relevant
                                                                                                                                                                                                                                                                                                            production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                production
                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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19

04-FEB-1991

(first

entry)

IgE binding factor

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RESULT 3
AAW13143
ID AAW1
XX
AC AAW1
XX
DT 17-J
DT 17-J
DT 17-J
DT 18-O
XX
Sequence 
RESULT 4
AAP70105
ID AAP7
XX
AC AAP7
XX
AC AAP7
XX
AC AAP7
XX
XX
IJE
DT 04-F
XX
DE IJE
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                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LYNC/) LYNCH R G.
(MATS/) MATSUI M.
(NUNE/) NUNEZ R M.
(YODO/) YODOI J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The specification states that the nucleotide sequences contained in figures 4a-b, 5a-b, 12a-12b and 13a-b are claimed, however this numbering scheme does not relate to the scheme used in the relevant sections of the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The cDNA encoding the present sequence, which contains human soluble CD23 isoform B, can be used for the large scale recoproduction of soluble CD23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA sequence encoding a soluble isoform scale preparation of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-159094/15
N-PSDB; AAT61956.
                                                                                                                       AAP70105;
                                                                                                                                                                    AAP70105 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Pages 18-20; 33pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JP09028385-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; soluble; CD23; complementarity determining;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence containing human soluble CD23 isoform B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW13143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW13143 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     isoform
                                                                                                                                                                                                                                                                                              117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90
                                                                                                                                                                                                                                                                                                                    1 ADLSSFKSQEL 11
                                                                                                                                                                                                                                                                                         ADLSSFKSQEL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADLSSFKSQEL
                                                                                                                                                                                                                                                                                                                                                                                        11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ₽,
                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      320 AA:
                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9408-0365103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95JP-0341169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90
                                                                                                                                                                    protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "soluble CD23 isoform
                                                                                                                                                                      321
                                                                                                                                                                                                                                                                                                                                                                                        0
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                                                                                                                                                                                                                                                                                                                                                                                                              Score 51;
Pred. No.
                                                                                                                                                                      Ā
                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₹
                                                                                                                                                                                                                                                                                                                                                                                                              0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of
                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CD23 -
                                                                                                                                                                                                                                                                                                                                                                                                                                     18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful for large
                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        recombinant
                                                                                                                                                                                                                                                                                                                                                                                        0
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ARESULT 5
AAP82073
ID AAP8
XX AAP8
XX AAP8
AC AAP8
XX IOW
CONT 17-C
XX IOW
XX I
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-APR-1986;
04-SEP-1986;
05-SEP-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The protein reacts with anti-Fc epsilon receptor antibody, and is obtd. In large quantities. The DNA encoding the protein is obtd. from, eg human B cells, human malignant B or T cells, human monocytes or human eosinophilic cells. RPMI 8866 cells may also be cultured to produce the mRNA. The IgE binding factor and Fc epsilon receptor binds IgE and can be used to enhance the prodn. of IgE from IgE producing cells. They can be used to treat allergies by eliminating excess blood IgE, and can also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; page 42-3; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1987-343202/49.
N-PSDB; AAN70107.
  Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Low affinity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAP82073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAP82073 standard; protein; 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New IgE binding factor protein - obtd. by culturing cells harbouring class specific Fc receptor on their surface.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Honjo T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KURS ) KURARAY CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-APR-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-DEC-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EP248211-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant Fc_epsilon receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IgE binding
                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 ADLSSFKSQEL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ADLSSFKSQEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yodoi J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             321 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86JP-0101531.
86JP-0209091.
86JP-0210429.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87EP-0106265
                                                                                /label-transmembrane region
/note-"hydrophobic residues"
63..63
  /label=glycosylation_site
/note="N-linked"
149..150
                                                                                                                                                             /label-stop_transfer_seq
/note-"basic cluster involved
integration into bilayer"
22..47
                                                                                                                                                                                                                                                                                                                                                                                                                                                        epsilon
                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11
                                                                                                                                                                                                                                                                                                /note="hydrophilic N-terminal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Takami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     epsilon receptor; allergy; RPMI 8866 cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 51; DB 8; Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        IgE; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                  in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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RRESULT 6
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding the sequence or a part of it can be used to make recombinant receptor which is useful for treating IgE allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 39; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human low affinity Fc(epsilon)-receptor and parts for treating local or systemic allergic reactions and recombinant DNA methods.
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P-PSDB; AAP82073.
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New human lower affinity Fc(epsilon)-receptor - useful for treating
                                                    WPI; 1988-057531/09.
N-PSDB; AAN81485.
                                                                                                                                  Kishimoto T,
                                                                                                                                                                                      (KISH/) KISHIMOTO T.
                                                                                                                                                                                                                                           21-AUG-1986;
                                                                                                                                                                                                                                                                                             21-AUG-1986;
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                                                                                                                                                                                                                                                                                                                                                                                                   EP257114-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Low affinity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-AUG-1986;
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11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fc_epsilon receptor; IgE; allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fc_epsilon receptor encoded by gene carried by pGEM4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                  Suemura
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/note="Claim 7"
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                                                                                                                                  Kikutani
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Pred. No. 0.12;
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Best Local S
Matches 11
                                                                                                                                                         Query Match
Best Local Similarity
Matches 11; Conserv
 Human IgE binding factor related polypeptide
                      12-DEC-1990
                                                                                                                                                                                                                     Fc epsilon receptor binds IgE. It is expressed from cell line RPMI8866. It is expressed in large ants, and can be used to remove excess IgE from blood, and to detect and quantify IgE. This would allow the development of therapy and diagnosis of allergy.
                                           AAP81112;
                                                              AAP81112 standard;
                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                            New DNA contg. nucleotide sequence encoding Fc epsilon receptor for obtaining IgE-binding substance used to detect and quantify IgE responsible for allergies.
                                                                                                                                                                                                                                                                                                                                                                                       05-SEP-1986;
24-APR-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JP63198988-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fc gamma receptor
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                                                                                                                                                                                                                                                                       Disclosure; ge 529; 16pp; japanese.
                                                                                                                                                                                                                                                                                                                                                  WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             17-AUG-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fc epsilon receptor; IgE; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAP81230;
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DB; AAN81612.
                                                                                                                 ADLSSFKSQEL 128
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Similarity 100.0%;
11; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 24;
                                                                                                                                                                                                    321 AA;
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                                                                                                                                                          Conservative
                     (first entry)
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87US-0042445
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                                                              peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reactions produced by the expression of IgE
                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English
                                                               321
                                                                                                                                                          0
                                                                                                                                                         Score 51; DB
Pred. No. 0.1
0; Mismatches
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Pred. No.
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                                                                                                                                                                   DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.12;
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                                                                                                                                                         Gaps
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AAP81172
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                     The peptide is related to the IgE receptors on human B-cells and, if without the membrane anchoring sequence, to the IgE-BFs of Sarfati et al. Immunology 53, 197, 207, 783 (1984).

Amino acids between 1-133 starting from the N-terminal may be deleted. This is the membrane-anchoring sequence binding the polypeptide to the cytoplasmic membrane of the B-cells.

Alternatively amino acids between 110-130 or 250-321 may also be deleted. The peptide has IgE binding activity and is useful tor treating allergic conditions, e.g. as caused by antigens such as pollens, cat danders and house dust mites.
11-APR-1987;
21-AUG-1986;
                                                                      EP259615-A.
                                                                                                                                            Sequence encoded by a gene for the water-soluble part of the human low affinity Fc-epsilon-receptor with the amino acids 150 to 321, comprising the EcoRI insert from pFc-epsilon-R-1.
                                                                                                                                                                                                            AAP81172;
                                                                                                                                                                                                                                AAP81172 standard; Protein; 321
                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
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N-PSDB; AAN81437.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-JUL-1986;
07-NOV-1986;
                              06-AUG-1987;
                                                   16-MAR-1988
                                                                                           Homo sapiens
                                                                                                               therapy.
                                                                                                                                                                                        28-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New IgE binding factor related polypeptide(s) - produced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-JUL-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-JAN-1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human IgE binding factor; IgE-BFs; allergic diseases; B-cells.
                                                                                                                        Low affinity Fc-epsilon-receptor;
                                                                                                                                                                                                                                                                                   118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              recombinant methods
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                                                                                                                                                                                                                                                                                                                          11;
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                                                                                                                                                                                                                                                                                                                                                                    321 AA;
                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                       (first entry)
87EP-0105425
86EP-0111581
                               87EP-0111392
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86GB-0026622
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Pred. No.
                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                          systemic IgE-allergic reaction;
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Best Local :
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05-DEC-1986;
06-AUG-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preparing FCR. Preferred embodiments of the present invention are psfc-epsilon-R-1 (see AAN81516/P81175) and also AAP81172. At least a part of the cDNA SQ coding for the AAS 1 to 148 of the FC-epsilon-R is replaced by a eucaryotic cDNA signal SQ e.g.an interleukin cDNA signal SQ e.g.by the BSF-2 signal SQ (see pBSF-2-L8-AAN81517/P81176). A suitable yeast expression vector is a plasmid contg. the yeast ADHI-promoter, a gene coding for the yeast mating factor alpha leader peptide (MF alpha leader SQ) a multicloning site and the yeast ADHI-terminator (see AAN81514/P81173). See also EP-258492.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The inventors claim a human low affinity Fc-epsilon-receptor (FCR) with an N-terminal cytoplasmic domain, a C-terminal extracellular domain and a mol.w. of about 46kd. Also claimed are recombinant DNA conty, the genetic information for the FCR, vectors conty, the DNA, host organisms transformed with the vectors, oligonucleotides coding for partial amino acid sequences from FCR, and processes for
                                                                                                                                                                                                                        Human lymphocyte receptor
asthma; immunoglobulin E;
                                                                                                                                                                                                                                                                                           01-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Table 3, Page 79-81; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant human low affinity Fc(epsilon)- receptor - used the treatment of local and systemic IGE-allergic reactions
 WPI; 1989-214148/30
                                                                                            20-JAN-1988;
                                                                                                                      20-JAN-1988;
                                                                                                                                                26-JUL-1989
                                                                                                                                                                        EP324879-A
                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                               Human lymphocyte receptor for immunoglobulin
                                                                                                                                                                                                                                                                                                                      AAP90120
                                                                                                                                                                                                                                                                                                                                              AAP90120 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (OSAU ) OSAKA UNIVERSITY. (KISH/) KISHIMOTO T.
                            Schwendenwein
                                                                 (OSAU ) OSAKA
                                                                                                                                                                                                                                                                                                                                                                                                              118 ADLSSFKSQEL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ADLSSFKSQEL 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                         (first entry)
                         Suemura M, Kikutani H, Barsumian R, Sommergruber W, Swetly P;
                                                                 UNIVERSITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Suemura M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86EP-0113073.
86EP-0116938.
87EP-0111392.
                                                                                            88EP-0100814
                                                                                                                      88EP-0100814.
                                                                                                                                                                                                                                                                                                                                             protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kikutani H,
                                                                                                                                                                                                                         for immunoglobulin;
lymphocyte receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                              321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 51;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                              Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barsumian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 9;
                                                                                                                                                                                                                                     hypersensitivity; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EL;
                                      EL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                       Schneider
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for
                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
RESULT 12
AAR42053
ID AAR42
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RESULT 11
AAP90367
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                QY
                                    Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Whole human lymphocyte receptor for immunoglobulin (see corresp. AAN90344). Used to produce highly bioactive water-soluble FCR. Water-soluble FCR binds IgE, so it is useful for treating hypersensitivity, esp. asthma. Amino acid residue 150 is a possible site for trypsin-like proteases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Soluble recombinant Fc-epsilon receptor - used for treatment or prophylaxis of local and allergic reactions induced by IgE.
                                                                                                                                 Cloned genes coding for soluble IgE receptor coding sequence of Fc epsilon receptor gene.
                                                                                                                                                            WPI; 1989-186101/26.
N-PSDB; AAN90134, AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; fig 1; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAN90344.
                                                                                                              Disclosure;
                                                                                                                                                                                                                                                                                      EP321601-A.
                                                                                                                                                                                                                                                                                                        Fc epsilon
                                                                                                                                                                                                                                                                                                                          Peptide sequence
                                                                                                                                                                                                                                                                                                                                             01-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                AAP90367
                                                                                                                                                                                                                                                                                                                                                                                AAP90367 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                         Sequence
                                                                                            The known
                                                                                                                                                                                         Kishimoto T,
                                                                                                                                                                                                                              22-DEC-1987;
                                                                                                                                                                                                                                                22-DEC-1987;
                                                                                                                                                                                                                                                                   28-JUN-1989
118
                                                                                                                                                                                                           (OSAU ) OSAKA UNIVERSITY
                                                                                                                                                                                                                                                                                                                                                                                                                                 118
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ADLSSFKSQEL 11
                  Н
ADLSSFKSQEL
                  ADLSSFKSQEL
                                                                                                                                                                                                                                                                                                                                                                                                                                ADLSSFKSQEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                           peptide sequence of Fc epsilon receptor gene
                                                                                                                                                                                                                                                                                                        receptor;
                                                                          321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          321 AA;
                                                                                                              fig 1;
                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                            (first
                                                                                                                                                                                        Suemura M,
                                                                          ξ
                                                                                                                                                                                                                              87EP-0119080
                                                                                                                                                                                                                                                87EP-0119080
                                                                                                                                                                                                                                                                                                                           of.
                                                                                                                                                             AAN90135, AAN90136
                                                                                                             19pp;
                                                                                                                                                                                                                                                                                                                           mutated
                                                                                                                                                                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                     cloned gene; IgE; allergy; ,asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                              100.0%;
                                                                                                              English
                                                                                                                                                                                         Kikutani H,
                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                           FC
                                                                                                                                                                                                                                                                                                                                                                                  321
                                             Score 51;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 51;
Pred. No.
                                                                                                                                                                                                                                                                                                                          epsilon
                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  ζ
                                                                                                                                                                                                                                                                                                                          receptor
                                                                                                                                                                                          Barsumian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10;
                                                       DB
                                                       10;
                                     0;
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                                                                                                                                           comprising modified
                                                       Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 321;
                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                     0;
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                                     Gaps
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AAR42053 standard; Protein; 321

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RESULT 13
AAW13142
ID AAW13
XX AAW13
XX 17-JU
AC AAW13
AC
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Best Local S
Matches 11
                                                                                                                                                         Key
Peptide
                                                                                                                                                                                                                                                                      Human; soluble; CD23; complementarity isoform A; recombinant production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence is of IgE-binding factor, secreted from the plasmid pSVG-BF. The plasmid pSVG-BF is a derivative of plasmid pSVG-ER which has the sequence coding amino acids 1-147 replaced with a coding region (AAQ55400) allowing secretion of the factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant DNA molecule - comprises enhancer and promoter unit
linked to transcriptive DNA segment and DNA segment comprising
promoter unit linked to DNA sub-segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
Region
  27-DEC-1995;
                                          04-FEB-1997
                                                                                         JP09028385-A
                                                                                                                                                                                                                              Homo
                                                                                                                                                                                                                                                                                                                                          Sequence containing human soluble CD23
                                                                                                                                                                                                                                                                                                                                                                                          17-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW13142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW13142 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 28; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1993-275121/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-DEC-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-DEC-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IL84702-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IgE; binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR42053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CIBA ) CIBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IgE binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADLSSFKSQEL 11
                                                                                                                                                                                                                              sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADLSSFKSQEL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 100.
l Similarity 100.
ll; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               321 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     factor.
                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GEIGY AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        factor;
  95JP-0341169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87IL-0084702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87IL-0084702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers 148..321 /label= IgE-binding
                                                                                                                                                              Location/Qualifiers
1..205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      secretion; expression; signal sequence.
                                                                                                                                      "soluble CD23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ige-binding_factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 51; DB
Pred. No. 0.1
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₹
                                                                                                                                      isoform
                                                                                                                                                                                                                                                                                              determining;
                                                                                                                                                                                                                                                                                                                                          isoform A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 14;
0.12;
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RESULT 14
AAP82839
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Best Local S
Matches 11
        This protein is useful in the treatment of local or systemic IgE-allergic reactions and is obtd. by recombinant DNA methods. pref. un-accompanied by associated native glycosylation. Fragit can also be used. See also AAN82253.
                                                               Disclosure; ;
                                                                                   New human low affinity Fc(epsilon)-receptor and parts - useful treating local or systemic IgE-allergic reactions and obtd. by recombinant DNA methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The cDNA encoding the present sequence, which contains human soluble CD23 isoform A, can be used for the large scale recombinant production of soluble CD23.

The specification states that the nucleotide sequences contained in figures 4a-b, 5a-b, 12a-12b and 13a-b are claimed, however this numbering scheme does not relate to the scheme used in the relevant sections of the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  \ensuremath{\mathsf{DNA}} sequence encoding a soluble isoform of CD23 scale preparation of the protein
                                                                                                                                 N-PSDB;
                                                                                                                                          WPI; 1988-065440/10.
                                                                                                                                                                 Kishimoto T,
                                                                                                                                                                                                             05-DEC-1986;
                                                                                                                                                                                                                                  05-DEC-1986;
                                                                                                                                                                                                                                                       09-MAR-1988
                                                                                                                                                                                                                                                                            EP258492-A.
                                                                                                                                                                                                                                                                                                Fc(epsilon)
                                                                                                                                                                                                                                                                                                                      Human low affinity Fc(epsilon)
                                                                                                                                                                                                                                                                                                                                                                   AAP82839;
                                                                                                                                                                                                                                                                                                                                                                                        AAP82839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Pages 16-17; 33pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-159094/15
N-PSDB; AAT61955.
                                                                                                                                                                                                                                                                                                                                             16-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MATS/) MATSUI M.
(NUNE/) NUNEZ R M.
(YODO/) YODOI J.
                                                                                                                                                                                       (CELL-) CELLULAR IMMUNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (LYNC/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-DEC-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 100.
1 Similarity 100.
11; Conservative
                                                                                                                                 AAN82252.
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                                                                                                                                                                                                                                                                                                                                                                                        standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   321 AA;
                                                                                                                                                                                                                                                                                                 receptor;
                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                               pp;
                                                                                                                                                                 Suemura
                                                                                                                                                                                                            86EP-0116938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94US-0365103.
                                                                                                                                                                                                                                   86EP-0116938
                                                               English.
                                                                                                                                                                                                                                                                                                                                                                                       protein;
                                                                                                                                                                 Z,
                                                                                                                                                                                                                                                                                                 low affinity; IgE-allergic reactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 09
                                                                                                                                                                 Kikutani H,
                                                                                                                                                                                                                                                                                                                                                                                         336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 51; DB Pred. No. 0.1); Mismatches
                                                                                                                                                                                                                                                                                                                       receptor.
                                                                                                                                                                                                                                                                                                                                                                                         ⋛
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 18;
0.12;
                                                                                                                                                                 Barsumian
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    useful for large

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                     Fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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                  of
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RESULT 15
ABB96396
ID ABB96396
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XX Gar
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Best Local S
Matches 11
    04-FEB-2000

24-FEB-2000

12-MAR-2000

16-MAR-2000

17-MAR-2000

19-MAY-2000

19-MAY-2000

19-MAY-2000

19-MAY-2000

11-JUL-2000

11-JUL-2000

11-JUL-2000

11-JUL-2000

11-JUL-2000

14-JUL-2000

14-JU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; testicular antigen; testes; cancer; metastasis; immune disorder; reproductive system disorder; urinary system disorder; gene therapy; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disease; infection; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human testicular antigen SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUN-2002 (first entry)
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|||||||||
8 ADLSSFKSQEL 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        336
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ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0214886.
2000US-0215135.
2000US-0216647.
2000US-0216880.
2000US-0217487.
2000US-0217496.
2000US-0218290.
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2000US-0186350
2000US-0189874
2000US-0190076
2000US-0190076
2000US-0198123
2000US-0209467
                        2000US-022964
2000US-0224519
2000US-0225213
2000US-0225266
2000US-0225266
2000US-0225267
2000US-022547
2000US-022547
2000US-0225757
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Pred. No.
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Search completed: March 13, 2003, 18:49:13 Job time: 30.2 secs
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                                                                                                                 Query Match 74.5%;
Best Local Similarity 80.0%;
Matches 8; Conservative
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01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                   The present invention provides the protein and coding sequences of 973 human testicular antigens, and fragments of their genomic sequences. The sequences can be used in the treatment of cardiovascular, urinary system, reproductive system, immune, respiratory, neurological and gastrointestinal disorders, infections, and particularly cancer, especially testicular cancers. The present sequence is a protein of the
                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding 973 human testicular antigen polypeptides, useful for preventing, diagnosing and/or treating testicular cancer
                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                           Claim 11; SEQ ID NO 1780; 766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-483232/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Rogen
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                                                                                                                                                                                                             invention.
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34 DLSSFKSGEI 43
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Pred. No. 4.8;
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Minimum DB seq length: 0
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Perfect score:
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Listing first 45 summaries
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US-09-971-317A-6
US-09-131-237-6
US-10-174-654-10
US-10-174-654-10
US-09-802-663-6
US-09-2027-287-6
US-09-929-493-6
US-09-929-110-1
2 US-10-012-452-13
2 US-10-012-452-13
2 US-10-012-452-13
2 US-10-017-910-5
0 US-09-899-059-6
0 US-09-899-059-6
0 US-09-193-663-4
US-09-711-171-4
0 US-09-711-71-359A-8
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53.938 Million cell updates/sec
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US-10-174-590-106	US-09-978-189-264	US-09-999-832A-264	US-10-066-500-121	US-09-978-192A-264	US-09-978-697-264	US-09-978-295A-264	US-09-833-435A-9	US-09-764-870-291	US-09-815-242-13624	US-09-815-242-13284	US-09-765-272-172	US-09-771-161A-188	US-09-815-242-13618	US-09-815-242-13365	US-09-933-999A-6	US-09-771-161A-97	US-09-801-368-346	US-09-815-242-13646	US-09-841-739-11	US-09-738-626-6798	US-09-886-241-6	-550-	US-10-007-693-73	US-09-841-132-523	US-09-765-272-10
106,	264,	264,	•	Sequence 264, App	•	264	9		Sequence 13624, A	13284	172,			Sequence 13365, A	Sequence 6, Appli	97, 1	Sequence 346, App	136	Sequence 11, Appl	679	Sequence 6, Appli	68	Sequence 73, Appl	Sequence 523, App	Sequence 10, Appl

ALIGNMENTS

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Sequence 6, Application US/08971317A Patent No. US20010010925A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Wiley, Steven R.
APPLICANT: Wiley, Steven R.
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDORESSEE: ABDORT ADDRESSEE: ABOOTT PARK ROAD
COTY: Abbott Park Road
COTY: Abbott Park
                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Goller, Mimic
REGISTRATION NUMBER: 39,046
REFERENCE/DOCKET NUMBER: 6255
TELECOMMUNICATION INFORMATION:
TELEPHONE: (847) 935-7550
TELEPAX: (847) 938-2623
                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08,
FILING DATE: 17-NOV-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                            SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
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OPERATING SYSTEM:
TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
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CURRENT APPLICATION NUMBER: US/09/131,237B
CURRENT FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: 60/074,047
EARLIER FILING DATE: 1998-02-09
EARLIER FILING DATE: 1998-01-09
EARLIER FILING DATE: 1998-01-09
EARLIER FILING DATE: 1998-01-09
EARLIER APPLICATION NUMBER: 08/461,246
EARLIER APPLICATION NUMBER: PCT/US94/12880
EARLIER APPLICATION NUMBER: PCT/US94/12880
EARLIER FILING DATE: 1994-11-07
NUMBER OF SEQ ID NOS: 24
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US-09-131-237-6
Sequence 6, Application US/09131237B
Publication No. US20030027284A1
GENERAL IMPORMATION:
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Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                   Sequence 10, Appropriate Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.0
SEO ID NO 6
LENGTH: 281
TYPE: PRT
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Best Local Similarity 100.
Matches 11; Conservative
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TITLE OF INVENTION: Tumor Necrosis Factor Gamma
FILE REFERENCE: PF141P3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Yu, Guo-Liang APPLICANT: Ni, Jian
                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      109 KELAELRESTS 119
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          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                         NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSE: Pharmacia & Upjohn, Intellectual Property
                                                                                                                                                                                                                                                Mills, Cynthia J
Jones, David A
TITLE OF INVENTION: TNF-Related Death Ligand
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                    APPLICANT: Bienkowski, Michael J
                                                                                                                                                 STREET: 301 Henrietta Street CITY: Kalamazoo
                                                                                                                  COUNTRY: USA
                                                                                                                                   STATE: MI
                                                                                                                                                                                                                                                                                                                                   Application US/10174654
No. US20030044937A1
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Pred. No. 0.051;
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TYPE: PRT
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; ORGANISM: Homo sapiens US-09-802-669-25
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Sequence 25, Application US/09802669
Patent No. US20020004490A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID US-10-174-654-10
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Best Local Similarity
Matches 11; Conserv
                                                                           Sequence 6, Application US/09193663 Patent No. US20020055624A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 11; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
APPLICANT: Wyatt, Jacqueline
APPLICANT: Zhang, Hong
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
FILE REFERENCE: ISPH-545
APPLICANT: Wiley, Steven R.
TITLE OF INVENTION: TNF-DELTA LIGAND AND USES THEREOF
FILE REFERENCE: 6255.US.02
CURRENT APPLICATION NUMBER: US/09/193,663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/802,669
CURRENT FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: US 09/665,615
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 09/290,640
PRIOR FILING DATE: 1999-04-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 180
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INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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109 KELAELRESTS 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 281 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Kerber, Lori L. REGISTRATION NUMBER: 41,113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/10/174,654 FILING DATE: 19-Jun-2002 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                     Conservative
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Pred. No.
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Pred. No. 0.051;
Mismatches 0
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CURRENT FILING DATE: 1998-11-17;
EARLIER APPLICATION NUMBER: 60/065,916;
EARLIER FILING DATE: 1997-11-17;
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 3.0;
SEQ ID NO 6
SEQ ID NO 6
LENGTH: 281
TYPE: PRT
ORGANISM: Homo sapiens
US-09-193-663-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Ebner, Reinhard

APPLICANT: Ruben, Steven M.

APPLICANT: Ullrich, Stephen

FIILE OF INVENTION: Apoptosis Inducing Molecule II

FILE REFERENCE: 1488.0650004

CURRENT FILING DATE: 1998-02-20

EARLIER APPLICATION NUMBER: US 09/003,886

EARLIER FILING DATE: 1998-01-07

EARLIER APPLICATION NUMBER: US 08/822,953

EARLIER APPLICATION NUMBER: US 60/030,157

EARLIER APPLICATION NUMBER: US 60/030,157

EARLIER FILING DATE: 1996-10-31

EARLIER FILING DATE: 1996-10-31

EARLIER FILING DATE: 1996-03-22

NUMBER: US 60/013,923
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US-09-027-287-6
                                                                                                                                                                                                                                                  US-09-252-656B-6
                                                                                                           Sequence 6, Application US/09252656B
Patent No. US20030081647A1
GENERAL INFORMATION:
APPLICANT: Ebner, Reinhard
APPLICANT: Ruben, Steven M.
APPLICANT: Ruben, Jun
APPLICANT: Zhang, Jun
APPLICANT: Zhang, Jun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 281
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Best Local Similarity
TITLE OF INVENTION: Apoptosis Inducing Molecule II FILE REFERENCE: 1488.0650006 CURRENT APPLICATION NUMBER: US/09/252,656B CURRENT FILING DATE: 1999-02-19
                                                                          APPLICANT: Zhang, Jun
APPLICANT: Ullrich, Stephen
APPLICANT: Zhai, Yifan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 55
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Pred. No.
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Pred. No.
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                                                          and Methods of
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; OTHER INFORMATION: Description of Combined DNA/RNA Molecule: n equals ; OTHER INFORMATION: a, t, g, or c US-09-929-493-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 6
LENGTH: 281
   Matches
                      Query Match
Best Local
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NUMBER OF SEQ ID NOS: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/234,338
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 60/240,806
PRIOR FILING DATE: 2000-10-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 2001-08-15
PRIOR APPLICATION NUMBER: 60/225,628
PRIOR FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: 60/227,008
PRIOR FILING DATE: 2000-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/929,493
CURRENT FILING DATE: 2001-08-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Neutrokine-alpha and Neutrokine-alpha Splice Variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/013,923
PRIOR FILING DATE: 1996-03-22
PRIOR APPLICATION NUMBER: US 60/030,157
PRIOR FILING DATE: 1996-10-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: PF343P4
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                                                                                                                                                                                                                  SOFTWARE: PatentIn
                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                  LENGTH:
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                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/276,248
FILING DATE: 2001-03-06
APPLICATION NUMBER: 60/293,499
FILING DATE: 2001-05-25
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/250,020 FILING DATE: 2000-11-30
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FILING DATE: 1998-02-20
APPLICATION NUMBER: US 09/003,886
FILING DATE: 1998-01-07
APPLICATION NUMBER: US 08/822,953
FILING DATE: 1997-03-21
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                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/296,122
                                                                                                                                                                                  281
                    Similarity
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Pred. No. 0.051;
                  Score 50; DB 10
Pred. No. 0.051;
   Mismatches
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   Indels
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Gaps
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1 KELAELRESTS 11

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RESULT 11
US-09-246-129B-6
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; TYPE: PRT
; ORGANISM: Homo sepiens
US-10-012-452-13
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-927-110-1
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Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                     Query Match
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TITLE OF INVENTION: VEGI, An Inhibitor of Angiogenesis and Tumor Growth
FILE REFERENCE: PF141P5
CURRENT APPLICATION NUMBER: US/10/012,452
CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: 09/559,290
PRIOR APPLICATION NUMBER: PCT/US98/23191
PRIOR APPLICATION NUMBER: PCT/US98/23191
PRIOR FILING DATE: 1998-11-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: PATY, Donald
APPLICANT: LUO, LIGING
TITLE OF INVENTION: METHOD FOR INHIBITING INFLAMMATION IN IMMUNE PRIVILEGED SITES USI
TITLE OF INVENTION: LIGAND FRAGMENTS
FILE REFERENCE: MBM1240
FILE REFERENCE: MBM1240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/927,110
CURRENT FILING DATE: 2001-08-10
                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 08/963,272
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                                                                          109 KELAELRESTS 119
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                                                                                                                                                 Local Similarity 100 tes 11; Conservative
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CYNADER, Max
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Pred. No. 0.051;
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Pred. No. 0.051;
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PRIOR FILING DATE: 2001-03-26
PRIOR PELING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/216,879
PRIOR APPLICATION NUMBER: 09/559,290
PRIOR APPLICATION NUMBER: 09/559,290
PRIOR APPLICATION NUMBER: 60/180,908
PRIOR APPLICATION NUMBER: 60/180,908
PRIOR FILING DATE: 2000-02-08
PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: 60/134,067
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: 60/132,227
PRIOR FILING DATE: 1999-05-03
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LENGTH: 278
TYPE: PRT
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PRIOR APPLICATION NUMBER: 09/131,237
PRIOR FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: 09/005,020
PRIOR APPLICATION NUMBER: 09/005,020
PRIOR FILING DATE: 1998-01-09
PRIOR APPLICATION NUMBER: 08/461,246
PRIOR FILING DATE: 1995-06-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/09899059 Patent No. US20020150534A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                 PRIOR
PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rosen, Craig A.
APPLICANT: Zhang, Jun
TITLE OF INVENTION: Tumor Necrosis Factor Gamma
FILE REFERENCE: PP141P7
CURRENT APPLICATION NUMBER: US/09/899,059
CURRENT FILING DATE: 2001-07-06
                                                                                                                   PRIOR
PRIOR
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CURRENT FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 60/074,047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: TUMOR N
FILE REFERENCE: PF141P4
    PRIOR
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NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: PCT/US94/12880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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APPLICATION NUMBER: 09/131,237 FILING DATE: 1998-08-07 APPLICATION NUMBER: 09/005,020
                                                                   APPLICATION NUMBER: 09/246,129
FILING DATE: 1999-02-08
APPLICATION NUMBER: 60/074,047
FILING DATE: 1998-02-09
                                                                                                                                                                 APPLICATION NUMBER: 60/131,963 FILING DATE: 1999-04-30
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PRIOR FILING DATE: 1995-06-05

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Best Local 9
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LENGTH: 278
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                                                                              Query Match
Best Local :
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PRIOR FILING DATE: 1994-11-07
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 279 amino acids
                                                                                                                                                                                                                                                                   NAME: Goller, Mimi C
REGISTRATION NUMBER: 39,046
REFERENCE/DOCKET NUMBER: 6255.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (847) 935-7550
TELEPAX: (847) 938-2623
                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/971,317A FILING DATE: 17-MOV-1997 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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TITLE OF INVENTION: THE DELTA LIGAND AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                           TOPOLOGY: 1: MOLECULE TYPE:
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                               1 KELAELRESTS 11
KELAELREFTN 117
                                                             Similarity .
9; Conservat
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Pred. No. 2.4;
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Pred. No. 2.
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RESULT 14
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US-09-193-663-4
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GENERAL INFORMATION:
APPLICANT: Wiley, Steven R.
APPLICANT: Wiley, Steven R.
TITLE OF INVENTION: TNF-DELTA LIGAND AND USES THEREOF
FILE REPERENCE: 6255.US.02
CURRENT APPLICATION NUMBER: US/09/193,663
CURRENT FILING DATE: 1998-11-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US Patent No. US20020159970A1 GENERAL INFORMATION:
                                                                                                                       Sequence 4, Application US/09193663 Patent No. US20020055624A1
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 279 amino acids
                                                                                                                                                                                                                                             107
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tes 9; Conserv
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TITLE OF INVENTION: A PROTEIN BELONGING TO THE THE SUPERFAMILY
INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC AC
METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: PHYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/447,035
FILING DATE: 1999-11-22
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Choi, Yongwon
                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Mus musculus SEQUENCE DESCRIPTION: SEQ ID NO: 5:
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                                                                                                                                                                                                                                             KELAELREFTN 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/10/017,910 FILING DATE: 14-Dec-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Hackensack
STATE: New Jersey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                      Conservative
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81.8%;
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Pred. No.
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## CARLIER APPLICATION NUMBER: 60/065,916
### CARLIER FILING DATE: 1997-11-17
### NUMBER OF SEQ ID NOS: 10
### SEQ ID NO 4
### SEQ ID NO 5
### SEQ ID NO 4
### SEQ ID NO 5
### SEQ
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Result
No.
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Maximum DB seq length: 200000000
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Perfect score:
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Match
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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        US-08-339-214-84
US-08-339-214-6
US-08-815-190A-2
US-08-815-190A-2
US-09-815-190A-2
US-09-157-864-10
US-08-339-214-26
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6, Appl
2, Appl
2, Appl
25, Appl
35, Appl
36, Appl
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37, Appl
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39, Appl
39, Appl
316, 
                                                                           ; NAME/KEY: Protein
; LOCATION: 1..178
; OTHER INFORMATION:
US-08-339-214-84
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 178 amino acid
                                                                                                                                                                                                                                       MOLECULE TYPE: FRAGMENT TYPE: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 11:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEPAX: 703-205-8050
                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
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178 amino acids

1110-139P

internal protein

100.0%;

Score 50;

DB 4; Length 178;

/note-

"polypeptide CD179"

RESULT 1 US-08-339-214 Sequence 84 Patent No. GENERAL APPLICAN TITLE OF FITTLE OF CORRESPO ADDRES STREET CITY: STREET COUNTR ZIP: COUNTR ZIP: COMPUTE MEDIUM COMPUTION SOFTMAT SOFTMA	22 22 23 23 23 24 24 24 25 26 27 27 28 28 28 28 28 28 28 28 28 28 28 28 28
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RESULT 3
US-08-339-214-6
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                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: amino acid
; STRANDENESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-649-100-9
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE_DOCKET NUMBER: 1110
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEPHA: (703) 205-8050
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 ADD 10 ADD 16
                                                                                                                                  Sequence 6, Application US/08339214 Patent No. 6348334
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Patent No. 6114507
                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
GENERAL INFORMATION:
APPLICANT: Nagata, Shigikazu
APPLICANT: Suda, Takashi
APPLICANT: Takahashi, Tomoniro
APPLICANT: Nakamura, No. 6348334io
TITLE OF INVENTION: A Fas Ligand, A
TITLE OF INVENTION: Encoding the Sa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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| 7 KELAELRESTS 17
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ZIP: 22040-0747
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CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 amino acids
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Pred. No. 0.037;
Mismatches
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); Mismatches 0;
                     A Fragment Thereof and DNA
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US-08-810-453-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Applica
Patent No. 5858990
GENERAL INFORMATIO
APPLICANT: Wals
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Matches
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 179 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/339
FILING DATE: 10-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MUTPHY Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: $1237/7004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)720-3500
TELEPAX: (617)720-2441
                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/810,453
                                                                                                                                                                                                                                                        COUNTRY: US
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: Federal Reserve Plaza, 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: FAS LIGAND COMPOSITIONS FOR TREATMENT OF TITLE OF INVENTION: PROLIFERATIVE DISORDERS
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CORRESPONDENCE ADDRESS:
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TOPOLOGY: linear
                                                                                                                              CLASSIFICATION:
                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 100.0%;
Local Similarity 100.0%;
les 11; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 22040-0747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: P.O. Box 7. CITY: Falls Church
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stewart, Kolasch & Birch
                                                                                                                                                                                                                                                         1110-139P
Score 50; DB 4;
Pred. No. 0.037;
0; Mismatches
                                    DB 4; Length 179;
Indels
0;
Gaps
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-810-453-2
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Best Local (
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                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                  TELEFAX: (415) 576-03 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                              NAME: Apple, Randolph T.

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 011823-006710US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/815,190A FILING DATE: 11-MAR-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Schneider, William F
APPLICANT: Vasquez, Maximiliano
                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                          FILING DATE: 13-MAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/614,584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
 109
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: San Francisco
                                                            Local Similarity es 11; Conserv
                                                                                                                                                                                   LENGTH:
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                             1 KELAELRESTS 11
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ilarity 100.0%;
Conservative
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Schneider, William P.
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ilarity 100.0%;
Conservative 0
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 0.059;
                                                         Score 50; DB 3; Pred. No. 0.059; Mismatches
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RESULT 6

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; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-290-640-25
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US-08-339-214-8
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Patent NO. 6263350
GENERAL INFORMATION:
APPLICANT: Barbera-Guillem, Emilio
TITLE OF INVENTION: Polynucleotides For Inhibiting Metastasis And Tumor Cell Grov
FILE REFERENCE: B-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
TITLE OF INVENTION: Antisense Compound Modulation
FILE REFERENCE: ISPH-0351
CURRENT APPLICATION NUMBER: US/09/290,640
CURRENT FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 85
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 25
                                                                                                                                                            Sequence 8, Patent No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 3
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                             Query Match
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CURRENT FILING DATE: 2000-01-07
EARLIER APPLICATION NUMBER: US 09/170,948
EARLIER FILING DATE: 1998-10-13
EARLIER APPLICATION NUMBER: US 60/062,733
EARLIER FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 28
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: WordPerfect
                                                                             APPLICANT:
APPLICANT:
APPLICANT:
          TITLE OF INVENTION: A TITLE OF INVENTION: En NUMBER OF SEQUENCES: 11 CORRESPONDENCE ADDRESS:
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ADDRESSEE:
                                                                                                                                                                                                                                                                                              1 KELAELRESTS 11
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                                                                                                                                                                6348334
                                                                                                                                                                            Application US/08339214
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                                                                             Takahashi, Tomoniro
Nakamura, No. 6348334io
                                                                                                            Nagata, Shigikazu
Suda, Takashi
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                             A Fas Ligand, A F. Encoding the Same: 103
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Stewart, Kolasch & Birch
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Pred. No.
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Pred. No. 0.059;
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                                                                 A Fragment Thereof and DNA
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Falls Church : Virginia

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US-08-339-214-30
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                                  APPLICATION NUMBER: US/08/339,214
FILING DATE: 10-MOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-139P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                                                                ZIP: 22040 COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:

1.30
COURSEL COMPATER COMPATE
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CITY: Falls Church
STATE: Virdinin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,214
FILING DATE: 10-NOV-1994
FILING DATE: 10-NOV-1994
CLASSIFICATION: 435
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NAME: Murphy Jr., Gerald M.
REGISTRATION UNMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-139P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TYPE: amino acid
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ZIP: 22040-0747
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22040-0747
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703-205-8050
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; OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
; OTHER INFORMATION: a, t, g, or c
US-09-589-287B-6
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US-09-157-864-10
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LENGTH: 281
TYPE: PRT
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Best Local Similarity
Matches 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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TITLE OF INVENTION: Antibodies to Neutrokine-alpha
FILE REFERENCE: P9343P3C1
CURRENT APPLICATION NUMBER: US/09/589,287B
CURRENT FILING DATE: 2000-06-08
                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prior application data removed - check PALM or file wrapper NUMBER OF SEQ ID NOS: 42\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                    APPLICANT: Mills, Cynthia J
APPLICANT: Jones, David A
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LENGTH: 281 amino acids
TYPE: amino acid
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NUMBER OF SEQUENCES:
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 APPLICATION NUMBER:
                                                                                                                                  COUNTRY:
                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                               ADDRESSEE: Pharmacia & Upjohn, Intellectual Property
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KELAELRESTS 11
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                                                                                                                                                                   Kalamazoo
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                                                                                                                                                                                   E: Legal Services
301 Henrietta Street
                                                                                                                                  USA
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                                                                                                                                                                                                                                                                                                                       Bienkowski, Michael J
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US/09/157,864
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Pred. No.
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Pred. No. 0.059;
Mismatches
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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-157-864-10
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                                              RESULT 13
PCT-US95-00362-2
                                                                                                                                                                                                                                                   ; OTHER INFORMATION: human wild-type Fas ligand (FasL) US-09-006-755B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Kang, Sang-Mo
APPLICANT: Braat, Andries E
APPLICANT: Baekkeskov, Steinunn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Stock, Peter G.
APPLICANT: The Regents of the University of California APPLICANT: The Regents of the University of California TITLE OF INVENTION: A No. 6451759cleavable Fas Ligand FILE REFERENCE: 18062K-000500US

. CURRENT APPLICATION NUMBER: US/09/006,755B

. CURRENT FILING DATE: 1998-01-14

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09006755B Patent No. 6451759
               Sequence 2, Application PC/TUS9500362 GENERAL INFORMATION:
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: DOMAIN
LOCATION: (103)..(281)
OTHER INFORMATION: extracellular domain
                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                              LOCATION: (119)..(154)
OTHER INFORMATION: metalloprotease recognition region
                                                                                                                                                                                                                                                                                                                                   NAME/KEY: PEPTIDE
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APPLICANT:
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nes 11; Conserv
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Local Similarity 100.0%;
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                                                                                                                                     1 KELAELRESTS 11
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IMMUNEX CORPORATION
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TORER: 41,113

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Pred. No.
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Pred. No. 0.059;
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US-08-815-190A-16
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Best Local :
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APPLICATION NUMBER: US 08,
FILING DATE: 07-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 01-FEB-1994
                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,190A
FILING DATE: 11-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, VC
CURRENT APPLICATION DATA:
CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Queen, Cary L.
APPLICANT: Schneider, William P.
APPLICANT: Vasquez, Maximiliano
APPLICANT: Vasquez, Esse 11 cand 1
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LENGTH: 281 amino acid
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STREET: Seattle
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                                                                                                                                                                                                                                 CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Anderson, Kathryn A REGISTRATION NUMBER: 32,1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: Apple Macintosh OPERATING SYSTEM: Apple 7
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Schneider, William P.
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06-JAN-1995
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REFERENCE/DOCKET NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 011823-006710US

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 287 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: TYPE: protein
US-08-815-190A-16
                                                                                                                                                                  CLASSIFICATION: 435

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Murphy, Matthew B.

REGISTRATION NUMBER: 39,787

REFERENCE/DOCKET NUMBER: 02307K-07100US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-576-0300

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CLARRATERISTICS:

LENGTH: 376 amino acids

TYPE: brotesin
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APPLICANT: Ramer, J. Kevin
APPLICANT: Williams, Lewis T.
TITLE OF INVENTION: Modified FAS Ligands
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
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US-08-751-512-8
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                                                                                  Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 11; Conservative 0
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Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 11; Conservative 0; Mismatches
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MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,512
FILING DATE: 15-NOV-1996
CIASCIETTCATTON: A25
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FILING DATE: 13-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T
RECISTRATION NUMBER: 36,429
RECISTRATION NUMBER: 36,429
204
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                    1 KELAELRESTS 11
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KELAELRESTS 214
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                                                                                                       Score 50; DB 3; Pred. No. 0.079;
                                                                                    Mismatches
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Search completed: March 13, 2003, 18:53:50 Job time: 10.8 secs

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Minimum I
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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YY199_YEAST
YY199_ADE07
MT16_BACSU
YOED_BACSU
YUE2_NEVOP
YRG5_CAEPL
YVCE_BACSU
YOCE_BACSU
ODFP_HUMAN
ODFP_BOVIN
ODFP_BOVIN
ODFP_BOVIN
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6 caenorhabdi
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7 bacillus su
6 chlamydia p
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6 myxococcus
                     7 aquifex aeo
methanobact
7 bacillus su
1 populus kit
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ALIGNMENTS

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EMBL; AF344847; AAK37606.1; HSSP; P01375; 4TSV. InterPro; IPR003636; TNF_abc. InterPro; IPR003636; TNF_family. InterPro; IPR00478; TNF_family. Pfam; PF00229; TNF; 1. PRINTS; PR01234; TNECROSISFCT. ProDom; PD002012; TNF; 1. SMART; SM00207; TNF; 1. PROSITE; PS00251; TNF_1; 1. PROSITE; PS00251; TNF_1; 1.	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	-!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By similarity)!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity)!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.	royrws, a receptor challed its. May be involved alls. May be involved in T cell developmen a role in the induct timulated suicide of m receptor TNFRSF6B/DcR	UENCE FROM N.A. SUE-Lymphocytes; LINE-21383618; PubMed-11491535; Linger F., Bostik P., Mayne A.E., King C.L., Gena in the second of the secon	TWEST6 OR FASE OR CD95L. TWEST6 OR FASE OR CD95L. Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Cercocebus. NCBI_TaxID=9531;		Capaily

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CARBOHYD
    This
                                                                                                                                                                                                                                                                                                 Kirii Y., Inoue T., Yoshino K.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a rece
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CD95L protein).

TNFSF6 OR FASL OR CD95L.

Macaca milatta (Rhesus macaque),

Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey),

Macaca nemestrina (Pig-tailed macaque).

Macaca nemestrina (Pig-tailed macaque).
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DOMAIN
SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES=M.mulatta; TISSUE=Lymphocytes; MEDLINE=21383618; pubMed=11491535; VIIInger F., Bostik P., Mayne A.E., King C.L., Weiss W.R., Ansari A.A.; Mayne A.E., Sting C.L., "Cloning, sequencing, and homology analysis of rest/Pas-11gand and co-stinulatory molecules."; immunogenetics 53:315-328(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cercopithecinae;
NCBI_TaxID-9544,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor ligand superfamily member 6
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                                                                                                                                                                                                                                                                                                                                                                     SPECIES=M.mulatta, M.fascicularis, and M.nemestrina;
Kirii Y., Inoue T., Yoshino K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteig
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                       transduces the apoptotic signal into cells. May be involved in cytotoxic T cell mediated apoptosis and in T cell development. TNFRSF6/FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T cells, or both. Binding to the decoy receptor TNFRSF6B/DCR3 modulates its effects (By similarity).

SUBCELLULAR LOCATION: Type II membrane protein and secreted 'Businilarity'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    μ
                                          PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).
SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY
                                                                                                                   similarity).
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    SWISS-PROT
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9541, 9545;
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80 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
MEMBER 6, MEMBRANE FORM.
  19
  copyright.
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N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
729EA60067B7D398 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 6, SOLUBLE FORM (BY SIMILARITY). CYTOPLASMIC (POTENTIAL). SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLEAVAGE (BY SIMILARITY). POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    macaque).
Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 50; DB 1;
Pred. No. 0.032;
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  is produced through a collaboration
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RESULT 3
TNF6_HUMAN
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Best Local
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CONFLICT
SEQUENCE
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PROSITE; PS00251; TNF_1; 1.

PROSITE; PS50049; TNF_2; 1.

Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.

Cytokine; Apoptosis; Transmembrane; Apoptosis; Ap
                                                                                                                                                                                                                                                                                                TNF6_HUMAN STANDARD; PRT; 281 AA. P48023; Q9BZP9; 01-FEB-1996 (Rel. 33, Created) 01-FEB-1996 (Rel. 33, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Tumor necrosis factor ligand superfamily member (Apoptosis antigen ligand) (APTL) (CD178 antigen TNFSF6 OR FASI OR APTLIGI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DOMAIN
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InterPro;
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EMBL; AB035138; BAA90295.1; -.
EMBL; AB035139; BAA90295.1; -.
EMBL; AB035140; BAA90296.1; -.
HSSP; P01375; 4TSV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                  MEDLINE-95127560; PubMed-7826947;
                                          SEQUENCE FROM N.A.
                                                                                 lymphocytes.
J. Exp. Med.
                                                                                                                                              Alderson M.;
                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE-95105731;
                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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11; Conservative
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IPR000478; TNF_family.
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N-LINKED (GLCNAC. ..) (POTENTIAL)
N-LINKED (GLCNAC. ..) (POTENTIAL)
S -> P (IN REF. 1).
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POLY-PRO.
CLEAVAGE
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Pred. No.
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EXTRACELLULAR
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Tanaka M., Ital T., Adachi M., Nagata S.;

"Downregulation of Fas ligand by shedding.";

Nat. Med. 4:31-36(1998).

"Ital T., Adachi M., Nagata S.;

Nat. Med. 4:31-36(1998).

"Ital Tensor of Fas ligand by shedding.";

Nat. Med. 4:31-36(1998).

"Ital Tensor of Cytokine that binds to TNFRSF6/FAS, a receptor that transduces the apoptotic signal into cells. May be involved in cytotoxic T cell mediated apoptosis and in T cell development.

"NNFRSF6/FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schneider P., Bodmer J.-L., Holler N., Mattmann C
Terskikh A., Peitsch M.C., Tschopp J.;
"Characterization of Fas (Apo-1, CD95)-Fas ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zeytun A., Nagarkatti M., Nagarkatti P.S.; "Isolation and characterization of a new naturally occuring variant human Fas ligand that is expressed only in membrane bound form.";
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Submitted
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Role of Fas ligand in apoptosis induced
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Human Fas ligand: specificity.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochem. Biophys. Res. Commun. 204:468-474(1994).
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splenomegaly.
- SIMILARITY: BELONGS TO
- DATABASE: NAME=PROW; I
WWW-"http://www.ncbi.i
                                                                                                                                                                                                                                                                                 SUBUNIT: HOMOTRIMER (PROBABLE).
SUBCELLULAR LOCATION: TYPE II MEMBRANE
INTO THE EXTRACELLULAR FLUID, PROBABLY
                                                                              lymphoproliferative syndrome (ALPS), syndrome (CSS), a childhood syndrome and thrombocytopenia with massive lym
                                                                                                                                            proteolytic processing.
DISEASE: Defects in TNFSF6 are a
                                                                                                                                                                                    PTM: N-glycosylated.
PTM: The soluble form
                                                                                                                                                                                                                                           SURFACE.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                             modulates its effects
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NOTE-PROW 2:59-69(2001)
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  .nlm.nih.gov/prow/guide/3338769674_g.htm".
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prodom; PD002012; TNF_abc; 1
SMART; SM00207; TNF; 1.
PROSITE; PS00251; TNF_1; 1.
PROSITE; PS50049; TNF_2; 1.
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Genew; HGNC:11936; TNFSF6.
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L; U08137; AAC50071.1; -.
L; U11821; AAC50124.1; -.
L; D38122; BAA07320.1; -.
L; AF288573; AAC60017.1; -.
L; 256050; CAB09424.1; -.
L; 250017502; AAH17502.1; -.
L; AB013203; BAA32542.1; -.
L; AB013203; BAA32542.1; -.
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IPR000478;
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CLEAVAGE.
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P->D, F, R: LOWERS BINDING TO
AND REDUCES CYTOTOXITY MORE
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N-LINKED (GLCNAC. ..) (POT
N-LINKED (GLCNAC. ..) (POT
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STSQMHTASSL -> ATPVHPLKKRS
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Pred. No.
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                                                                             SEQUENCE
                                                                                                                                  DISULFID
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HSSP: P01375; 4TSV.
InterPro; IPR003636; TNF_abc.
InterPro; IPR000478; TNF_family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBI outstation. European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way iffled and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transduces the apoptotic signal into cells. May be involved in cytotoxic T cell mediated apoptosis and in T cell development. TNFRSF6/FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3 modulates its effects (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).
SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity).
TISSUE SPECIFICITY: EXPRESSED IN ACTIVATED THYMOCYTES. MODERATE OR WEAK EXPRESSION FOL
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KELAELRESTS
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PS00251; TMF_2; 1.
PS50049; TMF_2; 1.
PS50049; Transmembrane; Glycoprotein; Signal-anchor. 1
PS50049; Transmembrane; Glycoprotein; Signal-anchor. 1
PS50049; TAMP TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FOR MEMBRANE FORM.
SUPERFAMILY
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                        Score 41; DB
Pred. No. 1.5;
1; Mismatches
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POLY-PRO.

CLEAVAGE (BY SIMILARITY).

POTENTIAL.

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N-LINKED (GLCNAC. . .) (POT

N-LINKED (GLCNAC. . .) (POT

N-LINKED (GLCNAC. . .) (POT
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EXTRACELLULAR
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                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL)
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Sciurognathi; Muridae
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P41047; Q61217; Q9RIF2;
Q1-FEB-1995 (Rel. 31, Created)
Q1-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
The recrosis factor ligand superfamily memb
"Polymorphism activity.";
Proc. Natl. Ac
                                                                                        Kayagaki N
Yagita H.;
                                                                                                                                                                                                                                                                             CHARACTERIZATION OF VARIANT GLD.
MEDLINE-96091792; pubmed-7495745;
Hahne M., Peitsch M.C., Irmler M.,
Rousseau M., Bron C., Renno T., Fre
"Characterization of the non-function.
Int. Immunol. 7:1381-1386(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20021694; PubMed=10552956;
Ayroldi E., D'Adamio F., Zollo O., Agostini M., Moraca R.,
Cannarile L., Migliorati G., Delfino D.V., Riccardi C.;
"Cloning and expression of a short Fas ligand: A new alternatively
spliced product of the mouse Fas ligand gene.";
Blood 94:3456-3467(1999).
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                                                                                                                                                                                    STRAIN-Various;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peitsch M.J., Tschopp J.J.;
"Comparative molecular modelling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-C57BI
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MEDLINE-94185175; PubMed-7511063;
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Mammalia; Eutheria; Rodentia; Sciurognathi;
                                                                                                                                                                                                                        /ARIANTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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76:969-976(1994).
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                                                                                                                                                                                                                     ALA-184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acids.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MAY-1996) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shioda T.,
                                                                                                                         Yamaguchi N.,
                                                              of murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32:761-772(1995).
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                                                                                                                                                                                                                                                                                                              C., Irmler M., Schroeter M., Lo, Renno T., French L., Tschopp the non-functional Fas ligand
                                                                                                                                                                                                                     GLY-218
   U.S.A. 94:3914-3919(1997)
                                                           Fas ligand that affects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isselbacher K.J
s ligand differs
                                                                                                                         Nagao F.,
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T., Smith C.A., Hunter
ated in gld mice and is
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                                                                                                                            Okumura
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Query Match
Best Local S
Matches S
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PROSITE; PS00251; TNF_1; 1.

PROSITE; PS00251; TNF_1; 1.

PROSITE; PS00251; TNF_2; 1.

Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor; Cytokine; Apoptosis; Transmembrane; Alternative splicing.

Cytokine; Apoptosis; Polymorphism; Alternative splicing.

Cytokine; Apoptosis; Polymorphism; Alternative splicing.

Cytokine; Apoptosis; Polymorphism; Alternative splicing.

Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor; Cytokine; Pacros LIGAND SUPERF MEMBER 6, MEMBERANE FORM.

CHAIN 1 279

MEMBER 6, MEMBERANE FORM.

CYTOKINE SUPERFIELD SUPERFIELD
                                                                                                                                                                                                                                                  CARBOHYD
VARSPLIC
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that transduces the apoptotic signal into cells. May be involved in cytotoxic T cell mediated apoptosis and in T cell development. TNFRSF6/FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T cells, or both. Binding to the decoy receptor TNFRSF6B/DCR3 modulates its effects (By similarity).

-i- SUBUNIT: HOMOTRIMER (PROBABLE).

-i- SUBCELLULAR LOCATION: Type II membrane protein (isoform FASL);
Secreted (isoforms FASL and FASL) FASL (SHOWN HERE) AND FASLS; ARE PRODUCED BY ALTERNATIVE SPLICING. ISOFORM FASL MEDIATES APOPTOSIS WHILE ISOFORM FASLS PREVENTS APOPTOSIS INDUCED BY FAS/FASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entitles requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                            SEQUENCE
                                                                                                                                        VARIANT
                                                                                                                                                                                    VARIANT
                                                                                                                                                                                                                             VARIANT
                                                                                                                                                                                                                                                                                              CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003636; TNF_abc.
InterPro; IPR000478; TNF_family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).

DISEASE: A DEFICIENCY IN THIS PROTEIN IS THE CAUSE OF GENERA LYMPHOPROLIFERATION DISEASE (GLD), AN AUTOSOMAL RECESSIVE DI RESPONSIBLE FOR LYMPHADEMOPATHY AND AUTOANTIBODY PRODUCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; U06948; AAA17800.1; -.
; U10984; AAA19778.1; -.
; S76752; AAB33780.1; -.
; U58995; AAB02915.1; -.
; AF119335; AAD52106.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERACTION
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    Similarity
9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PD002012; TNF_abc; 1.
                                                                                          279
    Conservative
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127
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                                                                                          31442 MW;
                    82.0%;
  Score 41;
Pred. No.
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 6, SOLUBLE FORM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                           -> A (IN STRAINS BALB/C AND DBA; NHANCES CYTOTOXICITY).
-> G (IN STRAINS BALB/C AND DBA;
                                                                                                                 SLI C
                                                                                          37972E2728E0A1CA CRC64;
    Mismatches
                                                                                                              (IN GLD; ABOLISHES BINDING RECEPTOR).
                                                                                                                                                                                                                                                  (IN ISOFORM FASLS)
                                                                                                                                                        CYTOTOXICITY)
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(GLCNAC. . .) (POTENTIAL).
(GLCNAC. . .) (POTENTIAL).
(GLCNAC. . .) (POTENTIAL).
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STRAIN-Guanxi bama mi.
Zhu N., Young Y.,
"Molecular cloning and
Submitted (APR-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9BEA8; Q95N10; Q95M04;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor ligand superfamily memb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-21322533; PubMed-11429161; Muneta Y., Shimoji Y., Inumaru S., Mox Muneta Y., Shimoji Y., Indexterization, "Molecular cloning, characterization, ligand (CD95 ligand)."; Interferon Cytokine Res. 21:305-312
EMBL;
                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                            "Porcine Fas-ligand gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   [4]
SEQUENCE FROM N.A.
STRDATN-Landrace x Large Yorkshire white;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tsuyuki S., Kono M., Bloom E.T.;
"Cloning and potential utility of porcine Fas
in porcine cells protects them from attack by
submitted (JUL-2001) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Lymphoid;
Tsuyuki S., Kono
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TNFSF6 OR FASL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                              . Immunol. 38:581-586(2002).

FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that transduces the apoptotic signal into cells. May be involved in cytotoxic T cell mediated apoptosis and in T cell development. TNFRSF6/FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3 modulates its effects (By Similarity).

SUBQUIT: Homotrimer (Probable).

SUBQUITE HOMOTRIMER (DCATION: Type II membrane protein and secreted (By SUBCELLIJLAR LOCATION: Type II membrane protein.
                                                                                                                                                                      proteolytic processing SIMILARITY: BELONGS TO
                                                                                                                                                                                                    PTM: The soluble form
                                                                                                                                                                                                                      INDUCTION: By IL-18.
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AB027297;
AY033634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
BAB40919.1;
AAK56449.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Nakajima Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         characterizaion of porcine Fas ligand cDNA.";
o the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                    derives
                                                                                                                                                                                                                                                                                                                                                                                                                      genomic
                                                                                                                                                                    derives from the membrane form by (By similarity).
THE TUMOR NECROSIS FACTOR FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Hoka S.,
                                                                                                                                                                                                                                                                                                                                                                                                                      sequence analysis and comparison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mor1 Y.; on, and expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Thymocytes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ligand: overexpression human cytolytic cells."; databases.
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EMBL; HSSP;

AF397407; AAK84408.1; AB069764; BAB64291.1;

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RC STRAIN-VC-16 / DSM 4304 / ATCC 49558;

RX MEDLINE-98049343; PubMed-9389475;

RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

RA Klenk M.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

RA Klenk M.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

RA Klenk M.-P., Clayton R.A., Gwinn M., Hickey E.K., Peterson J.D.,

RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,

RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

RA Citcon R., Gocayne J.D., Weldman J.F., McDonald L., Utterback T.,

RA Cotton M.D., Spriggs T., Artlach P., Kaine B.P., Sykes S.M.,

RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,

M. Wenter J.C.;
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matches
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ProDom: PD002012; TNF_abc; 1.
SMART; SM00207; TNF; 1.
PROSITE; PS00251. ***-
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CARBOHYD
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DOMAIN
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                                       "The complete genome sequence of reducing archaeon Archaeoglobus Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
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InterPro; IPR000478; TNF_family.
Pfam; PF00229; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Archaea; Euryarcháeota; Archaeoglob1; Archaeoglobaceae; Archaeoglobaceae; Archaeoglobus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Archaeoglobus fulgidus.
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                      CATALYTIC ACTIVITY:
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|KELTELRESAS
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81.8%;
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82 TUMOR NECROSIS FACTOR LIGAND SUPERF
                   ATP +
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Pred.
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N-LINKED (GLCNAC. . .) (POTENTIAL)
F -> L (IN REF. 4).
T -> P (IN REF. 2).
; 6743DAA1145671FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEMBER 6, SOLUBLE FORM (BY SIMILARITY).
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED
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                      succinate +
                                                                               of the
                                                       t the hyperthermophilic, sulphate-
fulgidus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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1 (EC 6.2.1.5) (SCS-beta 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      382 AA
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                      ADP
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-1992 (Rel. 2
01-NOV-1995 (Rel. 3
16-OCT-2001 (Rel. 4
Immediate-early reg
                                                                                                                                                                   Ayres M.D.,
"The complet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIGNI; FIGURE TIGRO1016; SUCCOADETA; I.
TIGRENA'S; TIGRO1016; SUCCINYL_COA_LIG_3; 1.
PROSITE; PS01217; SUCCINYL_COA_LIG_3; 1.
Ligase; Tricarboxylic acid cycle; Complete proteome.
Ligase; Tricarboxylic acid cycle; Complete proteome.
An An A2204 MW; 418ACBA41E64DA9F CRC64;
                                                     VIFOLOGY 202:586-605(1994).

1: FUNCTION: IE-N AUTOREGULATES ITS OWN EXPRESSION AND STIMULATES BOTH IE-1 AND IE-0 IN TRANSIENT ASSAYS. THE STIMULATION OF IE-: EXPRESSION MAY ACCOUNT FOR THE AUGMENTING ACTIVITY OF IE-N IN IE-1 MEDIATED TRANS-ACTIVATION OF THE 39K PROMOTER.

1: SIMILARITY: TO OPMINY IMMEDIATE-EARLY PROTEIN IE-2.

-:- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                   Carson D.D., Summers M.D., Guarino L.A., "Molecular analysis of a baculovirus reg Virology 182:279-286(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a copyright the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                        This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                      "The complete DNA sequence polyhedrosis virus.";
                                                                                                                                                                                 MEDLINE-94303173; PubMed-8030224; Ayres M.D., Howard S.C., Kuzio J.,
                                                                                                                                                                                                                                                                                                                                                               Viruses; dsDNA viruses, Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VIEN_NPVAC
P24647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003135; ATP-grasp.
InterPro; IPR000303; CoA_ligase.
Pfam; PF00549; ligase-CoA; l.
Pfam; PF02222; ATP-grasp; l.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P07460; 2SCU.
TIGR; AF1540; -.
               between
                                                                                                                                                                                                              STRAIN-C6;
                                                                                                                                                                                                                                                                                                                                                                                           Autographa californica nuclear
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-!- SUBUNIT: Composed of an alpha chain
                                                                                                                                                                                                                                                                                              MEDLINE=91220660; PubMed=2024466;
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=46015;
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity).
SIMILARITY: BELONGS
FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
8; Conser
               the
                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 21, Created)
(Rel. 32, Last sequence update)
(Rel. 40, Last annotation update)
arly regulatory protein IE-N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
 Swiss Institute of Bioinformatics Bioinformatics Institute. There a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.0%;
88.9%;
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                                                                                                                                                                   uzio J., Lopez-Ferber M., of Autographa californica
                                                                                                                                                                                                                                                                                                                                                                           lear polyhedrosis virus (AcMNPV).
RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                 regulatory gene.";
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7.7;
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Best Local s
Matches 8
                                                                                                                                                                      STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZN_FING
CONFLICT
SEQUENCE
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InterPro; IPRO01841; Znf_ring
Pfam; PF00097; Zf-C3HC4; 1.
SMART; SM00184; RING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
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PROSITE; PS50089; ZF_RING_2; 1.
Early protein; Transcription regulation; Transcription; DNA_binding.
Activator; Repeat; Zinc-finger; DNA_binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                     Zerler B., Myers P.A., Escalante H., Roberts R.J.;
Unpublished observations (XXX-1997)
-i- fUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE GGNCC.
-i- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give specific double-stranded fragments with terminal 5'-phosphates.
                                                                                                                                                                                                                                                                                                                                                                                                                                               258844;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Activator; Repeat; DOMAIN 9
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                                                                                                                                                                 "Complete genome sequence jannaschii.";
                                                                                                                                                                                                                                                                                                                                                                                                                            Methanococcus jannaschii.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                     CHARACTERIZATION.
                                                                                                                                                     Science
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                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=2190;
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X 4 AA TANDEM REPEATS
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InterPro; IPR003439; ABC_transportr
Pfam; PF00005; ABC_tran; 2.

PROSITE; PSO Hypothetical

protein;

ATP-binding; Transmembrane; Glycoprotein;

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01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
15-JUL-1999 (Rel. 38, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hilbert H., Moestl D.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. PDR5 SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Z71685; CAA96352.1; -. EMBL; Z71686; CAA96354.1; -. SGD; S0005353; YNR070W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions on modified and this statement is not removed. Usage by and for commendenties requires a license agreement (See http://www.isb-sib.ch/annouentities requires a license agreement a license agre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Andre B., Iraqui Houssaini I., Urrestarazu L.A., Vissers Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
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Pred. No.
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Almedda J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
Champan J.C., Clamp M., Clark G., Clark N.N., Clark S.Y., Clee C.M.,
RA Chapman J.C., Clamp M., Clark G., Clark N.N., Clark S.Y., Clee C.M.,
RA Clegs S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clegs S., Cobley V.E., Collier R.E., Connor L.E., Corby N.R.,
RA Clegs S., Cobley V.E., Collier R.E., Connor D., Dunn M.,
RA Clegs S., Cobley V.E., Collier R.E., Connor D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Hammond S., Harley J.L., Heath P.D., HO S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jokosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lehvaslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Milne S.A., Mistry D., Moore M.J.E., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
BA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
BA Oliver M. Ramsay H., Schrank R. Schranken P. Sime S.
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Nomura N., Ohara O.;
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MEDLINE=21638749; PubMed=11780052;
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Mammalia; Eutheria;
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SYI_MYCTU STANDARD;
Q10765; O06181;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence upd.
16-OCT-2001 (Rel. 40, Last annotation upd.)
                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-98295987; PubMed-9634230;

Gold S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris

Gordon S.V., Eighmeier K., Gas S., Barry C.E. III, Tekaia F.,

Gordon S.V., Eighmeier K., Gas S., Barry C.E. III, Tekaia F.,

Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

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STRAIN-CDC 1551 / Oshkosh;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Fleischmann R.D., Alland D., Eisen M.L., Haft D., Hickey E., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                         Nature
[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-H37Rv;
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Bacteria; Actinobacteria;
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RESULT 13
YQBO_BACSU
ID YQBO_B
AC P45931
DT 01-NOV
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DE HYPOTH
GN YQBO.
OS Bacil1
OC Bacter
OX NCBI_T
RN [1]
RP SEQUEN
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01-NOV-1995
15-JUN-2002
                                                                                                                                                            STRAIN-168 / JH642;
MEDLINB-95219086; PubMed-7704261;
Takemaru K.-I., Mizuno M., Sato T., Takeuchi M., Kobayashi
"Complete nucleotide sequence of a skin element excised by
rearrangement during sporulation in Bacillus subtilis.";
Microbiology 141:323-327(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPR002300; tRNA-Synt_1a.
Interpro; IPR001412; tRNA-Synt_I.
Interpro; IPR002301; tRNA-Synt_ile
pfam; PF00133; tRNA-Synt_1; 1.
PRINTS; PR00804; TRNASYNTHILE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
-!- CATALYTIC ACTIVITY: ATP + L-isoleucine + tRNA(Ile)
STRAIN=168 / JH642;
MEDLINE=97124195; PubMed-8969508;
Mizuno M., Masuda S., Takemaru K.
Kobayashi Y.;
"Systematic sequencing of the 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Metal-binding; Zinc; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bishai W.;
"Whole genome comparison
                                                                                                                                                                                                                                                                                                                                                                                      Bacillus subtilis.
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YQBO_BACSU
P45931;
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diphosphate + L-isoleucyl-trna(lle).
COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
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MT1587; -.
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622
1041
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(Rel. 32, Last sequence update)
(Rel. 41, Last annotation update)
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70.0%;
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    of the 283 kb 210 degrees-232 degrees region
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MW;
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"KHSKS" REGION.
"KHSKS" REGION.
ATP (BY SIMILARITY).
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Pred. No.
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                                                    K.-I., Hosono S.,
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                                                    Sato T., Takeuchi M.,
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                                                                        Matches
                                                                                               Best
                                                                                                               Query Match
                                                                                                                                                   EMBL; D32216; BAA06947.1; -.
EMBL; D84432; BAA12411.1; -.
EMBL; Z99117; CAB14544.1; -.
Subtitist; BG11286; yqbo.
InterPro; IPR000189; SLT_domain.
Pfam; PF01464; SLT; 1.
Hypothetical protein; Complete pr
SEQUENCE 1585 AA; 171030 MW;
                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fc entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the Bacillus subtilis genome containing the skin element and many sporulation genes."; Microbiology 142:3103-3111(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         This
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-!- SIMILARITY: STRONG, TO B.SUBTILIS XKDO.
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Kunst F., Ogasawara N., Moszer I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     computer system prototype.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Medigue C., Moszer I., Viari A., Danchin A.;
"Analysis of a Bacillus subtilis genome fragment using a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96084975; PubMed=7489895;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDENTIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 390:249-256(1997).
253 KALAELTESSS 263
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                                   1 KELAELRESTS
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8; Conser
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RESULT 14
HEX9_ADEQ
ID HEX9]
AC P0321
DT 21-JJ
DT 21-JJ
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DE Hexon
OS Humman
OC Virum
OX NCBI,
RN [1]
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P56859;
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                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
90-MAY-2000 (Rel. 39, Last annotation update)
Phosphoadenosine phosphosulfate reductase (EC 1.8.99)
reductase, thioredoxin dependent) (PADOPS reductase)
phosphoadenylylsulfate reductase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The nucleotide sequence of the polypeptide IX gene of human adenovirus type 3."; Gene 13:387-394(1981).
-I- FUNCTION: THIS PROTEIN IS A STRUCTURAL COMPONENT OF THE VIRION.
MAY HAVE AN ADDITIONAL ROLE DURING ADENOVIRUS MULTIPLICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. SPECIES-Human adenovirus type 3; MEDLINE-81261949; PubMed-7262560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIES-Human adenovirus type 7; STRAIN-Gomen;
MEDLINE-81261948; PubMed-6266923;
Dijkema R., Maat J., Dekker B.M.M., van Ormondt H., Boyer H.W.;
"The gene for polypeptide IX of human adenovirus type 7.";
Gene 13:375-385(1981).
                                           SEQUENCE FROM
                                                                                                                                                 Eurotiales; Trichocomaceae;
                                                                                                                                                                                                                               Emericella nidulans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMENI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A03854; SXAD97.
PIR; B03854; SXAD93.
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21-JUL-1986 (Rel. 01,
15-DEC-1998 (Rel. 37,
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   MEDLINE-95287864;
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6; Conserv
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                                                                                                                                                                                    ns (Aspergillus nidulans).
Ascomycota; Pezizomycotina;
   PubMed-7770049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.0%;
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                                                                                                                                                         Emericella
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MOI. Gene. 247:423-429(195).
-i- FUNCTION: THE NADP DEPENDENT REDUCTION OF PAPS INTO SULFITE INVOLVES THIOREDOXIN WHICH PROBABLY PLAYS THE ROLE OF A THIOL
                                                                                                                                  EMBL; X82555; -; NOT_ANNOTATED_CDS.
InterPro; IPR002500; PAPS_reduct.
InterPro; IPR004511; cysH.
Pfam; PF01507; PAPS_reduct; 1.
TIGRFAMs; TIGR00434; cysH; 1.
Methtonine blosynthesis; Cysteine blosynthesis; SEQUENCE 293 AA; 33978 MW; FCBB379183F21D5F
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use by non-profit institutions as long as its content is in
modified and this statement is not removed. Usage by and for con
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                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration
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10
                                N
                                                                                                                                                                                                                                                                                                                                                                                                              LEADS TO THE BIOSYNTHESIS OF METHIONINE AND CYSTEINE.
SIMILARITY: BELONGS TO THE PAPS REDUCTASE FAMILY. CYSH SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                         PATHWAY: THIRD STEP IN THE LEADS TO THE BIOSYNTHESIS
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ETAELRDST 18
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77.8%;
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hypothetical prote hypothetical prote hypothetical prote probable ileS prot phage-related prot variant-specific s hexon-associated phexon-associated protranscription regular pyruvate dehydroge sapc protein, benol sohB protein, pept probable choline k succinate-CoA liga
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KELAELRESTS 11

Query match Best Local S Matches 11	A;Gene: Fasi A;Introns: 151 A;Introns: gl C;Keywords: gl F;80-102/Domai F;76,184,250,2	A; Molecule typ A; Molecule typ A; Residues: 1- A; Cross-refere C: Genetics:	A;Title: Fas 1 A;Title: Fas 1 A;Reference nu A;Accession: II A:Status: nrel	A;Status: prel A;Molecule typ A;Residues: 1- A;Cross-refere R;Alderson, M.	A; Molecule typ A; Residues: 1- A; Cross-refere R; Schatzlein, submitted to t A; Reference nu	A; Residues: 1-281 <res> A; Cross-references: EMBL:U1 R; Mita, E.; Hayashi, N.; I1 Biochem. Biophys. Res. Comm A; Title: Role of Fas ligand A; Reference number: JC2340; A; Accession: JC2340</res>	RESULT 1 138707 Fas ligand - human C; Species: Homo sapiens (man) C; Date: 29-May-1998 #sequence. C; Accession: I38707; JC2340; (R; Takahashi, T.; Tanaka, M.; Int. Immunol. 6, 1567-1574, 11 A; Title: Human Fas ligand: get A; Reference number: I38707; M A; Accession: I38707 A; Status: preliminary; transla A; Molecule type: mRNA		33333333333333333333333333333333333333
100. imilarity 100. ; Conservative	/1; 116/3 ycoprotein; tran n: transmembrane 60/Binding site:	e: mRNA 281 <re2> nces: EMBL:U08137;</re2>	0 70 10	iminary e: mRNA e: mRNA 281 <sch> nces: EMBL:X89102; nces: Tough, T.W.; C</sch>		281 <res> nces: EMBL:U118 yashi, N.; Iio, ys. Res. Commun of Fas ligand ii mber: JC2340; M</res>	g n n n		66.0 405 66.0 413 66.0 444 66.0 491 66.0 494 66.0 494 66.0 576 66.0 576 66.0 576 66.0 583 66.0 1101 66.0 1186
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281; s 0; Gaps	#status predict	1; PID:g624628	in human T lymph	Falk, B.; Schooley,	PIDN:BAA07320.1; P	; PID:g595431 Kasahara, A.; C virus infec	nge 21-Jul-2000 Nagata, S. ion and species		immediate early pr immediate early pr hypothetical prote cell wall-binding ABC transporter. s probable carboxy t carboxy terminal p hypothetical prote hypothetical prote ct288 hypothetical conserved hypothet hypothetical prote ct288 hypothetical conserved hypothet hypothetical prote hypothetical prote carbamoylphosphate carbamoylphosphate
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G; Accession: C69442

R; Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Fleischmann, R.D.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.
                                                         Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J. Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P. Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Tittle: The complete genome sequence of the hyperthermophilic, A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: C69442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fas ligand - mouse (house mouse) C;Species: Mus musculus (house mouse) C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999 C;Accession: A53062 R;Takehashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; R;Takehashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.;
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A53062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fas ligand - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 13-Jan-1995 #sequence_revision 13
C:Accession: A49266
                                                                                                                                                                                                                                                                       succinyl-CoA synthetase, beta subunit (sucC-1) homolog - Archaeoglobus fulg
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 16-Jul-1999
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A;Residues: 1-279 <TAK>
A;Cross-references: GB:U0694B; NID:g473564; PIDN:AAA17800.1; PID:g473565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: A53062; A; Accession: A53062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R:Takahashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Cell 76, 969-976, 1994
A;Title: Generalized lymphoproliferative disease in mice, A;Reference number: A53062; MUID:94185175; PMID:7511063
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S. Cell 75, 1169-1178, 1993
A;Title: Molecular cloning and expression of the Fas ligand, A;Reference number: A49266; MUID:94084792; PMID:7505205
A;Accession: A49266
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A49266
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A; Molecule
A; Residues:
                                       A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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A; Residues: 1-278 <SUD>
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Best Local (
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                 type: DNA
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9; Conserv
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81.8%;
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81.8%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                     K.E.; Ketchum, K.A.; D
G.; Gill, S.; Kirkness,
J.F.; McDonald, L.
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A;Cross-references: GB:AE000996; GB:AE000782; NID:g2689319; PIDN:AAB89706.1; C;Superfamily: succinate-CoA ligase (ADP-forming) beta chain
  2;
Length 383
                                                                                  PID: 9264
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              Ş
                                Matches
                                              Query Match
220 ELAELREAT 228
                              Local Similarity
nes 8; Conserv
               2 ELAELREST 10
                               Conservative
                                      76.0%;
88.9%;
                                       Score 38;
Pred. No.
                                Mismatches
                                     DB
16;
                                0
                                Indels
                               0
                                Gaps
                               0
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MIVIA RESULT

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A:Cross-references: GB:M59422; NID:g332437; PIDN:AAA46701.1; PID:g332438 C;Superfamily: AcMNPV immediate-early protein IE-N C;Keywords: DNA binding; early protein; tandem repeat; transcription regulation F;34-49/Region: 7-residue repeats
F;51-58/Region: 4-residue repeats
                                                                                                                                                                                                                                                                                                                                 Virology 182, 279-286, 1991
A;Title: Molecular analysis
A;Reference number: A39150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    immediate-early protein IE-N - Autographa californica nuclear polyhedrosis virus
C;Species: Autographa californica nuclear polyhedrosis virus, AcMNPV
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-408 < CAR>
                                                                                                                                                                                                                                                                                                                A; Accession: A39150
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                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: A39150
                                               Matches
                                                                  Query Match
Best Local
                                                                                                                                 190-196/Region: glutamine-rich
1 KELAELRESTS 11
                                            Similarity 72.
                                                                                                                                                                                                                                                                                                                                                                                                            Summers, M.D.; Guarino, L.A.
                                                                    74.0%;
72.7%;
                                                                                                                                                                                                                                                                                                                                          of a baculovirus regulatory MUID: 91220660; PMID: 2024466
                                                                  Score 37;
Pred. No.
                                               Mismatches
                                                                    DB
27;
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                                                                                       Length 408
                                               Indels
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                                            0
                                               Gaps
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311 KELSELRAKTS 321
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R;Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D. Virology 202, 586-605, 1994
A;Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis A;Reference number: A72850; MUID:94303173; PMID:8030224
A;Accession: A72869 A;Note: dsDNA virus C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 11-Jan-2000 early gene transactivator - Autogacy; Species: Autographa californica A; Molecule type: DNA A; Residues: 1-408 < AYR> A; Status: preliminary C; Accession: A72869 Autographa californica nuclear polyhedrosis virus ornica nuclear polyhedrosis virus, ACMNPV

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                                                        A; Gene: Ac-IE-2
C; Superfamily: ACMNPV immediate-early protein IE-N
                                                                            C; Genetics:
                             Query Match
Best Local
                    Matches
                            Local
 1 KELAELRESTS 11
                                                                     AC-IE-2
                   Similarity
8; Conserv
                    Conservative
                            74.0%;
                            Score 37;
Pred. No.
                    Pred. No. 27;
; Mismatches
                               DB
27;
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                    ۲,
                                       Length 408;
                    Indels
                    0;
                    Gaps
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A;Cross-references: GB:L22858; NID:g510708; PIDN:AAA66781.1;

PID: 9559220

밁 311 KELSELRAKTS 321

RESULT 7 A59292 probable type ï myosin heavy chain slime mold (Physarum polycephalum) (fragment)

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A; Residues: 1-317 <BAI>
A; Residues: 1-317 <BAI>
A; Cross-references: GB:AJ133501; NID:g4494062; PIDN:CAB39170.1; PID:g4494063
A; Experimental source: strain CL; dev stage plasmodium formation; clone lib to C; Genetics:
A; Gene: mynD
C; Superfamily: kinetoplast-associated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein MJ1449 - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: H64480
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Meinstock, K.G.; Merrick, J.M.; Glodek, rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasca, Reference number: A64300; MUID:96337999; pMID:8688087
A;Accession: H64480
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C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change
C;Accession: A59292
R;Bailey, J; Cook, L.J.; Kilme.Barber, R.; Swanston, E.; Solnic
submitted to GenBank, March 199
A;Description: Identification of three genes expressed primaril;
A;Paterion enumber: A59292
A;Accession: A59292
A;Status: preliminary; not compared with conceptual translation
A;Status: preliminary;
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R;Stover, C.K.; Pham, X.O.; Erwin, adman, S.; Yuan, Y.; Brody, L.L.;
                                                                                                                                                                                                                                                                           probable carboxyl-terminal proteinase PA5134 [imported] - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                         A; Molecule type: DNA
A; Residues: 1-436 <STO>
                                                                                           A;Title: Complete genome se
A;Reference number: A82950;
A;Accession: B83005
                                                                                                                                                               .; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
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A; Residues: 1-370 < BUL>
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A;Cross-references: GB:AE004926; GB:AE004091; NID:g9951424; PIDN:AAG08519.1; GSPDB:GN001
                                                                        A; Status: preliminary
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nes 7; Conserv
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                                                                                                                     sequence of Pseudomonas aeruginosa PA01,
50; MUID:20437337; PMID:10984043
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ch 1999
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Pred. No.
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A.; Larbig,
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K.; Lim,
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dek, A.
                                                                                                                                                                                                                                                                                                                       (strain
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A; Gene:
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  A;Map position: 14R
C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding
C;Reywords: ATP- nucleotide binding; P-loop; transmembrane protein
F;46-257/Domain: ATP-binding cassette homology <ABCl>
                                                                                                                                                                                                                              submitted to the Protein St A; Reference number: S62944 A; Accession: S63402
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                                                                                                                     C; Genetics:
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A;Reference number: A71250;
A;Accession: E71297
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6; Conservative
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A;Molecule type: DNA
A;Residues: 1-1333 <AND>
A;Residues: 1-1333 <AND>
A;Cross-references: EMBL:Z71685; NID:g1302603; PIDN:CAA96352.1; PID:e239601; PID:g130
A;Experimental source: strain S288C
A;Experimental strain S288C
A;Experimental source: strain S288C
A;Experimental strain S28
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R;Andre, B.; Iraqui Houssaini, I.; Urrestarazu, L.A.;
submitted to the Protein Sequence Database, April 1996
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N;Alternate names: hypothetical protein N3568
C;Species: Saccharomyces cerevisiae
C;Date: 27-Apr_1996 #sequence_revision 03-May-1996 #text_change 19-Apr-2002
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A; Cross-references: GB: AE001240; GB: AE000520; A; Experimental source: strain Nichols
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A; Residues: 1-1053 < DUE>
A; Cross-references: EMBL: Z71685; MIPS: YNR070w
A; Experimental source: strain S288C
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Pred. No. 1e+02;
4; Mismatches
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A; Gene: PH0907
C; Superfamily:
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A; Residues: 1-159 <KAN>
A; Residues: 1-159 <KAN>
A; Cross-references: GB:AP000004; NID:g3236131; PIDN:BAA30001.1;
A; Experimental source: strain OT3
A; Note: this accession replaces an interim accession for a seque C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       K:Kawarabayasi, Y.; Sawada, M.;
M.; Ohfuku, Y.; Funahashi, T.;
DNA Res. 5, 55-76, 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic A;Reference number: A71000; MUID:98344137; PMID:9679194 A;Accession: C71080
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A; Residues: 1-74 <STO>
A; Cross-references: GB
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7; Conserv
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8; Conserv
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                                                                                            Score 34;
Pred. No.
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Pred. No.
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Pred. No. 2.3e+02;
l; Mismatches 2;
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Hough, D.W.; Maddocks,
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Search completed: March 13, Job time: 13.8 secs

2003, 18:52:55

time :

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synemin - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 03-Nov-2000
C;Accession: I50721
R;Becker, B.; Bellin, R.M.; Sernett, S.W.; Huiatt, T.W.; Robson, R.M.
Biochem. Biophys. Res. Commun. 213, 796-802, 1995
Biochem. Biophys. Res. Commun. 213, 796-802, 1995
A;Title: Synemin contains the rod domain of intermediate filaments.
A;Reference number: I50721; MUID:95382823; PMID:7654240
A;Accession: I50721
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I50721
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                                                                                                                                                         A;Cross-references: EMBL:U28143; NID:g1052880; PID:g1052881 C;Superfamily: cytoskeletal keratin
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A; Introns: 33/2; 74/3;
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A;Experimental source: strain Bristol N2; clone C40A11
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-294 <MAG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, October 1998 A;Description: The sequence of C. elegans cosmid A;Reference number: 221374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein C40All.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 *sequence_revision 29-Oct-1999 *text_change 29-Oct-1999 C;Accession: T33588 R;Maggi, L.; Goela, D.
                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-304 <BEC>
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Maximum DB seq length: 2000000000
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Perfect score;
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re greater than or equal to the score of the result being point
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T. Takahashi T;					ctor family; apopt n; Fas-L; CD179; t	as ligand CD179.			178 AA.	ALIGNMENTS	AAR79095	AAR79069 AAR79066	AAR88356	AAY87572	ABB05000 AAW27146	AAU04556 ABB81652	AAY87582	AAY87580	AAY87578	AAY87576	AAY87574	AAB19342 AAY87569	AAW98071 AAW95041	AAY28594	AAW49105	AAW27143	AAR79097	AAY 04 3 / 2 AAR 77 28 1	AAY28595	AAW48953 AAY28596
				,	osis; cell death; runcated.						S	Fas ligand in	Fas ligand.	H3/FasL dom	Fas ligand as ligand do	Fas ligand Fas ligand	n Fas ligand	Fas ligand	n Fas ligand	Fas ligand	Fas ligand	acid sequen	<u>-</u>	:ype Fas lig Fas ligand	Fas ligand. Igand. Mamm	Fas ligand.	n Fas ligand. n Fas ligand	as-I	s ligand (FasL)	Non-cleavable Fas Fas ligand (FasL)

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13-DEC-1993;
18-MAR-1994;
08-JUL-1994;
07-SEP-1994;
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                                                             Sequence
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N-PSDB; AAQ94157.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR79099 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide which binds to Fas antigen, and antibody reactive with it for treatment and diagnosis of viral or auto:immune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                              (OSAB-)
                                                                                                                                                                                                                                                                                                                                                                                                                               (MOCH )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7
                                                                                            ligands or active fragments able to induce apoptosis ch express the Fas cell surface antigen are claimed. T telns are isolated from human, rat and mouse sources, uence represents part of the human Fas ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ligand; Tumour Necrosis factor family; apoptosis; cell death; cell surface antigen; Fas-L; human.
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OSAKA BIOSCIENCE
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                                                                                                                                                                                                      Page 222-224;
                                                               179
                                                                                                                                                                                                                                                                                                                                                                    Nakamura
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94JP-0180955
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0.054;
                                                                                                                                                                                                                                              antibody reactive with auto:immune diseases
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RESULT 3
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                                                                                                                                                                                                                         Antibody reactive with Fas ligand capable of iused for diagnostic assay of Fas ligand in bootreatment of diseases in which Fas ligand/Fas
                                                                                                                                                                                   Disclosure; Fig 1; 164pp;
                                                                                                                                                                                                                                                                                                            WPI; 1997-108917/10.
                                                                                                                                                                                                                                                                                                                                                                                          (MOCH )
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30-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human: Fas ligand; antigen; neutral; antibody; apoptosis; induction; assay; enzyme linked immunosorbant assay; diaggisease; hepatitis B; hepatitis C; human immunodeficiency graft versus host disease; ulcerative colitis; sequelae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fas ligand
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OSAKA BIOSCIENCE
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95JP-0188480
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89..107
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60..72
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79..89
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47..60
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/label=
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164..174
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                                                                                                                                                                                                                         inducing apoptosis -
dy fluids and for
antigen is involved
                                                                                                                                                                                                                                                                                                                                                    Vasquez
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Antigens derived from the present human Fas ligand sequence can be used in the preparation of a neutral antibody against an apoptosis inducing Fas ligand. The antibody can be used in a Fas ligand assay, e.g. an enzyme linked immunosorbant assay, to diagnose diseases in which the Fas ligand/Fas antigen system is implicated, e.g. hepatitis B/C, human immunodeficiency virus, graft/host disorders, ulcerative colitis or sequelae of myocardi infarction. The antibody may also be used to treat such diseases

myocardial diseases.

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RESULT 4
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Heteromeric complexes comprising lymphotoxin sub-units - us inhibitors of signalling by TNF- and TNF-related receptors, treating auto:immune disease, graft rejection. etc.
                                                                                                                                                                                                           07-JUN-1995;
                                                                                                                                                                                                                                                                                                                             W09640774-A1
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11; Conserv
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172
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68..70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence comprises the C-terminal extracellular domain of the Fas ligand altered to drive trimerisation with wild-type lymphotoxin (LT)-beta. LT subunit association domains potentiate subunit associations into an active trimeric ligand. Tumour necrosis factor (TNF)-related ligand monomers mutated in their respective subunit associations domains can form heteromeric complexes with LT subunits. LT-alpha/beta heteromeric
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Misc-difference 129..130
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171..172
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88..89
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145..146
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68..70
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177..17
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94
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Best Local S
Matches 11
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                             30-DEC-1999;
                                                                                       DE19963859-A1
                                                                                                                    Unidentified
                                                                                                                                           Fusion protein; dimerization; oligomerization; Clq; vaccine; diphtheria; collectin; antiinflammatory; immunomodulatory; antiapoptotic; apoptotic; antiviral; antibacterial; antimalarial; antiprotozoal; antitumor; BCG; endocrinological; medicine; autoimmune disease; hyper-apoptotic state; hypo-apoptotic state; infection; tumor; endocrinological disorder; immunization; rubella; measles; poliomyelitis; rables; tetanus; malaria; yellow fever; human immune deficiency virus; influenza.
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                                                          12-JUL-2001
                                                                                                                                                                                                                                                                   Fast fusion construct Fast-hexamer.
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                                                                                                                                                                                                                                                                                                                                                           AAB86306 standard;
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CC bound signaling molecules or receptors or is an antibody (or its containing molecules or receptors or is an antibody (or its containing as component B CC aprotein of the Clq or collectin families; (b) DNA sequences (II) that CC encode the FP of (a); (c) expression vectors containing (III); (d) host CC cells containing the vector of (c); and (e) (II) in which component B of CP is derived from the immunoglobulin, Clq or collectin families of proteins. The products of the invention have antiinflammatory, antiprotozoal, antitumor and endocrinological activity. (I) CC antimalarial, antiprotozoal, antitumor and endocrinological activity. (I) CC are useful, in human or veterinary medicine, to: (i) produce pharmaceuticals for treatment of inflammation; autoimmune diseases; (particularly of the lymphatic system) and/or endocrinological disorders; (ii) produce vaccines for active or passive immunization against CC infections (specifically rubella, measles, poliomyelitis, rables, CC virus or influenza), also as vaccine adjuvants; or (iii) for in vitro CC diagnosis. Crosslinking of component A is now achieved without requiring CC activity and regeneration of activity. This sequence represents the Fasi CC trimer construct described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes novel dimers or oligomers (I) of di-, tri-, tetra- or penta-mers (II) of recombinant fusion proteins (FP) comprising tetra- or penta-mers (II) of recombinant fusion proteins a loilogically active protein (or fragment) and B is a protein (or fragment) that causes dimerization/oligomerization of (I) without regulring a third molecule. Particularly A functions as a ligand for antibodies, soluble or membrane
Sequence
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  213
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RESULT 7 밁 Ş AAB86307; AAB86307 standard; protein; 213 41 1 KELAELRESTS 11 KELAELRESTS 5

13-SEP-2001

(first entry)

Matches Query Match Best Local

Local Similarity

100.0%;

Score 50; DB Pred. No. 0.0 0; Mismatches

DB 22; 0.066; 0

Length Indels

213; 0

Gaps

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Conservative

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Fusion protein; dimerization; oligomerization; Clq; vaccine; diphtheria; collectin; antiinflammatory; immunomodulatory; antiapoptotic; apoptotic; antiviral; antibacterial; antimalarial; antiprotozoal; antitumor; BCG; Unidentified endocrinological; medicine; autoimmune disease; hyper-apoptotic st hypo-apoptotic state; infection; tumor; endocrinological disorder; immunization; rubella; measles; poliomyelitis; rabies; tetanus; ma yerrow Fast fusion construct super-Fast. fever; human immune deficiency virus; influenza; super-FasL malaria; state;

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                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   particularly A functions as a ligand for antibodies, soluble or membrane bound signalling molecules or receptors or is an antibody (or its fragment). The invention also describes (a) FP containing as component B a protein of the Clq or collectin families; (b) DNA sequences (II) that encode the FP of (a); (c) expression vectors containing (III); (d) host cells containing the vector of (c); and (e) (II) in which component B of FP is derived from the immunoglobulin, Clq or collectin families of FP is derived from the invention have antilinflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes novel dimers or oligomers (I) of di-, tri-, tetra- or penta-mers (II) of recombinant fusion proteins (FP) comprising at least one each of components A and B, where A is a blologically active protein (or fragment) and B is a protein (or fragment) that causes dimerization/oligomerization of (I) without requiring a third molecule.
                                   Human; Fas ligand; Fas ligand-fusion protein; leucine zipper; transmembrane protein; hepatotropic; immunosuppressive; apopt liver cell necrosis; viral hepatitis; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New dimers or oligomers of oligomeric recombinant useful as pharmaceuticals and vaccines, comprises and component that induces oligomerization -
                                                                                                             FLAG peptide-Leucine zipper-human Fas ligand fusion protein.
                                                                                                                                                     20-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     super-FasL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (APOT-) APOTECH RES & DEV LTD
                                                                                                                                                                                                                               ABB05003 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2;
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                                                                                                                                                                                                                                                                                                                             41
                                                                                                                                                                                                                                                                                                                                                                   1 KELAELRESTS 11
                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     construct described in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 18-19; 42pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 213 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                       Score 50;
Pred. No.
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functional component
                                                     apoptosis;
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RESULT 9
AAY28597
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     which contains all or part of the Fas ligand sequence, a peptide capable of forming an oligomer and a peptide which increases the production yield of recombinant protein. The fusion protein contains: (1) a FLAG peptide sequence; (2) an leucine zipper sequence; and (3) the extracellular domain of human Fas ligand. The fusion protein has hepatotropic and immunosuppressive activities. Binding of the Fas ligand sequence to Fas on the surface of cells expressing Fas induces apoptosis in the cells. The fusion protein can be used in the treatment of diseases with which Fas expressing cells are associated, such as liver cell necrosis produced by viral hepatitis, and autoimmune diseases. The present sequence represents a fusion protein of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; Page 46-48; 48pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fusion proteins of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-097655/13.
N-PSDB; ABA92524.
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                                                                                   Misc-difference
                                                                                                                        Synthetic.
                                                                                                                                                            autoimmune destruction; cleavage site; mutein
                                                                                                                                                                      Fas ligand; FasL; apoptosis; non-cleavable; graft intolerance;
                                                                                                                                                                                                Fas ligand (FasL) mutant delta
                                                                                                                                                                                                                         26-NOV-1999
                                                                                                                                                                                                                                                  AAY28597;
                                                                                                                                                                                                                                                                          AAY28597 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                      22-JUL-1999
                                             WO9936079-A1
                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention.
                                                                                                                                                                                                                                                                                                                                                                                                Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention describes a fusion protein comprising a peptide
                                                                                                                                                                                                                                                                                                                                       KELAELRESTS
                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    teins of a Fas ligand with an oligomer promoter peptide, useful for inducing Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                       238
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                                                                                                                                                                                                                        (first entry)
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                                                                        /note-
                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                      "Deletion of 20 wild-type amino acids (126-145)"
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               forming peptide and an apoptosis in cells
                                                                                                                                                                                                                                                                                                                                                                                                              Length 238;
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07-JAN-1999;

99WO-US00667.

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RESULT 10
AAW48954
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence is Fas ligand (FasL) mutant delta 3. This protein was made by deleting amino acids 126-145 (inclusive) of the wild-type FasL sequence AAV28594. The FasL protein activates the Fas receptor which indices apoptosis. The FasL deletion mutants (AAV28595-Y28597) are non-cleavable. The mutations inhibit the proteolytic cleavage of FasL and have the capacity to activate a Fas receptor-mediated pathway.

Claimed mutants of FasL or an organ or tissue expressing a mutant can be used to alleviate symptoms of a fas receptor-mediated by inadequate or inappropriate stimulation of a Fas receptor-mediated pathway, such as the proteorist, in a tissue or organ. In particular, FasL mutants can be used to treat intolerance to a graft in a patient. The FasL mutants protect can organ or tissue from autoimmune destruction.

CC Note: The present sequence is not shown in the specification but it has been derived from the wild-type FasL sequence AAV28594 shown in the
                                                                                                                                                                                                                                                                                                                                                Key
Region
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                                   13-NOV-1997;
                                                                                          22-MAY-1998.
                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Backkeskov S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Non-cleavable Fas ligand 1306145 deletion mutein; Fas; erythematosus; gene therapy; autoimmune disease; multiple sclerosis; heumatoid arthritis; myasthenia gravis; transplant rejection;
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ilarity 100.0%;
Conservative (
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1..129
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                                                                                                                                                                                                 represents residues 146-281 wild-type Fas ligand"
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Pred. No. 0.082;
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Best Local
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13-NOV-1996;
10-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                  Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glomerulonephritis.
  12-NOV-1997;
13-NOV-1996;
                                                                                    13-NOV-1997;
                                                                                                                                                                                                                                                                                                                   Region
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rheumatoid ar
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                                                                                                                                            22-MAY-1998
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ilarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fas ligand 1306142 deletion mutein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-0968686.
96US-0030871.
97US-0039972.
97US-0968686.
96US-0030871.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORP.
                                                                                    97WO-US20864
                                                                                                                                                                                                                                                                                                                   130..268
                                                                                                                                                                                                                                                                                                                                             /note-
                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                        "represents residues 143-281 of wild-type Fas ligand"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₹
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The present sequence represents a non-cleavable Fas ligand 1306145 deletion mutain. Fas ligand deletion mutein can be expressed in cells transfected with the DNA (AAV32623) coding for the mutant protein. These cells, expressing the mutant Fas ligand in a non-cleavable form, are claimed to be useful in vitro to identify cells that express Fas and, in vivo or in vitro, for reducing proliferation of Fas-expressing cells. The DNA encoding the Fas ligand mutant is claimed to be useful in gene therapy procedures and for the treatment of autoimmune diseases, e.g. multiple sclerosis, erythematosus, rheumatoid arthritis, glomerulonephritis, myasthenia gravis and transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New DNA encoding Fas ligand agonist including, e.g. deletion useful for, e.g. treating auto-immune diseases or transplant
Score 50; DE
Pred. No. 0.0
); Mismatches
                            0.084;
                                                                    B
                                                                 19;
0
                                                                 Length 265;
   Indels
0
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       These cells, expressing the mutant Fas ligand in a non-cleavable form, are claimed to be useful in vitro to identify cells that express Fas and, in vivo or in vitro, for reducing proliferation of Fas-expressing cells. The DNA encoding the Fas ligand mutant is claimed to be useful in gene therapy procedures and for the treatment of autoimmune diseases, e.g. multiple sclerosis, erythematosus, rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a non-cleavable Fas ligand 1306142 deletion mutein. Fas ligand deletion mutein can be expressed in cells transfected with the DNA (AAV22622) coding for the mutant protein.
A non-cleavable Fas ligand polypeptide Fas receptor-mediated apoptosis
                                                                                                                               07-JAN-1999;
                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                             Fas ligand;
                                                                                                                                                                                                                                                                                                                   Fas ligand (Fasi) mutant delta
                                                                                                                                                                                                                                                                                                                                           26-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                  AAY28596
                                                                                                                                                                                                                                                                                                                                                                                       AAY28596 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                glomerulonephritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Pages 62-63; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New DNA encoding Fas ligand agonist including, e.g. deletion useful for, e.g. treating auto-immune diseases or transplant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAV32622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                    WPI; 1999-468942/39
                                                                                 (REGC ) UNIV CALIFORNIA
                                                                                                        14-JAN-1998;
                                                                                                                                                    22-JUL-1999
                                                                                                                                                                           WO9936079-A1
                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                  autoimmune destruction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KELAELRESTS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1998-297861/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                 KELAELRESTS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          268 AA;
                                                                                                                                                                                                                                                                                 FasL; apoptosis; non-cleavable; graft intolerance;
destruction; cleavage site; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                        98US-0006755
                                                                                                                               99WO-US00667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0039972
                                                          Braat D,
                                                                                                                                                                                                             Location/Qualifiers 125..126
                                                                                                                                                                                                  /note-
                                                                                                                                                                                                                                                                                                                                                                                        Protein; 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               myasthenia gravis and transplant rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                "Deletion of 10 wild-type amino acids
                                                          Kang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 50;
Pred. No.
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                                                          Stock
          that has capacity to activate
                                                          PG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.085;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 268;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                 (126-135)
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RESULT 13
AAY28595
ID AAY28
XX AAY28
XX AAY28
AC Fas 1
KW Fas 1
KW Fas 1
KW Autoi
XX Homo
OS Synth
XX Homo
OS Synth
XX AUToi
XX A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence is Fas ligand (FasL) mutant delta 2. This protein was made by deleting amino acids 126-135 (Inclusive) of the wild-type FasL sequence AAY28594. The FasL protein activates the Fas receptor which induces apoptosis. The FasL deletion mutants (AAY28595-Y28597) are non-cleavable. The mutations inhibit the proteolytic cleavage of FasL and have the capacity to activate a Fas receptor-mediated pathway. Claimed mutants of FasL or an organ or tissue expressing a mutant can be used to alleviate symptoms of a disorder characterized by inadequate or inappropriate stimulation of a Fas receptor-mediated pathway, such as apoptosis, in a tissue or organ. In particular, FasL mutants can be used to treat intolerance to a graft in a patient. The FasL mutants protect an organ or tissue from autoimmune destruction.

Note: The present sequence is not shown in the specification but it has been derived from the wild-type FasL sequence AAY28594 shown in the
This sequence is Fas ligand (FasL) mutant delta 1. This protein was n by deleting amino acids 126-129 (inclusive) of the wild-type FasL sequence AAY28994. The FasL protein activates the Fas receptor which induces apoptosis. The FasL deletion mutants (AAY28595-Y28597) are
                                                                                                                                                                                A non-cleavable Fas ligand polypeptide Fas receptor-mediated apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fas ligand;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY28595;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        specification.
                                                                                                                                     Example
                                                                                                                                                                                                                                                                                                                   Baekkeskov S,
                                                                                                                                                                                                                                                                                                                                                                    (REGC ) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                       14-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9936079-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fas ligand (FasL) mutant delta 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY28595 standard; Protein; 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KELAELRESTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POCGIT
                                                                                                                                                                                                                                                                     1999-468942/39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
                                                                                                                               1; Page -; 81pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       destruction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FasL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                       CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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X
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                                                                                                                                                                                                                                                                                                                   Braat D,
                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0006755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US00667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
125..126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       apoptosis; non-cleavable; graft intolerance;
ction; cleavage site; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Deletion of 4 wild-type amino acids
                                                                                                                               English.
                                                                                                                                                                                                                                                                                                                   Kang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                      Stock
                                                                                                                                                                                                              that has capacity to
                                                                                                                                                                                                                                                                                                                      ස
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.086;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 271;
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                                                                                                                                                                                                                 activate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (126-129)*
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                                                                                 made
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RESULT 14
AAY04372
ID AAY04372
XX AAY04
XX AAY04
XX AAY04
XX Human
XX Human
XX Human
XX Human
XX Human
XX Vira
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                        The present sequence is a protease-resistant Fas ligand derivative in which a region of human Fas ligand which is susceptible to protease attack has been deleted. The present invention also describes apoptosis modulators containing soluble Fas ligand. The modification in the Fas ligand renders it resistant to the action of proteases such as the metalloproteinase which in vivo cleaves the active membrane-bound Fas ligand (which is active as an apoptosis inducer). The Fas ligand can be used for the prevention and treatment of diseases such as cancer, viral infection and autoimmune disease, e.g. by introduction of DNA encoding the modified Fas ligand into effector cells using a suitable gene
                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Page 48-49; 60pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-229531/19.
N-PSDB; AAX33117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; Fas ligand derivative; antagonist; apoptosis modulator; apoptosis inducer; cytotoxic activity; protease resistant; can viral infection; autoimmune disease; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    non-cleavable. The mutations inhibit the proteolytic cleavage of FasL and have the capacity to activate a Fas receptor-mediated pathway. Claimed mutants of FasL or an organ or tissue expressing a mutant can be used to alleviate symptoms of a disorder characterized by inadequate or inappropriate stimulation of a Fas receptor-mediated pathway, such as apoptosis, in a tissue or organ. In particular, FasL mutants can be used to treat intolerance to a graft in a patient. The FasL mutants protect an organ or tissue from autoimmune destruction.
                                 therapy vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protease-resistant Fas ligand derivatives used for prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KELAELRESTS 11
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OSAKA BIOSCIENCE
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11; Conservative
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Matches 11
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                                                       Sequence
                                                                         expressed
                                                                                 screened with a murine Fas-L probe. Isolated clones were amplified by PCR, and a desired fragment ligated into vector pBluescript SK. The cDNA insert of recombinant vector Fas-L/pBS, deposited as E. coli ATCC 69527, is given in AAQ91311. Recombinant Fas-L was
                                                                                                                                       Claim 3; Page 25-27; 38pp; English.
                                                                                                                                                                  Human and murine DNA encoding ligand(s) binding to cell surface protein Fas - useful for studying auto-immune disorder(s) and development of
                                                                                                                                                                                              N-PSDB; AAQ91311
                                                                                                                                                                                                       WPI; 1995-255032/33.
                                                                                                                                                                                                                         Goodwin
                                                                                                                                                                                                                                          (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                             01-FEB-1994;
07-JAN-1994;
                                                                                                                                                                                                                                                                                        06-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                                                                                                                                     Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                      A cDNA library prepd. from human peripheral blood lymphocyte mRNA was
                                                                                                                                                         self-tolerance.
                                                                                                                                                                                                                                                                                                          13-JUL-1995
                                                                                                                                                                                                                                                                                                                             W09518819-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fas ligand; Fas-L;
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KELAELRESTS 11
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                            Similarity
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                                                                         in CV1-EBNA-1 cells.
                                                       281 AA;
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                   Conservative
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94US-0179138
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80
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Pred. No.
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                                   Length 281;
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109

KELAELRESTS 119

Search completed: March 13, 2003, 18:49:12 Job time: 30.2 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                         score greater than or equal to the score of the result bein and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.
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| length:
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1: /SIDS1/gcgdata/g
2: /SIDS1/gcgdata/g
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Gapop 10.0 , Gapext 0.5
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/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
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Score	Query Match	Query Match Length DB		ID	Description
 40	88.9	9	22	ABP12751	
40	88.9	9	22	ABP17961	
40	88.9	10	23	ABB80017	
40	88.9	10	23	AAE19118	
40	88.9	10	23	AAU75795	
40	88.9	11	22	ABP17190	
40	88.9	11	23	AAU80096	
40	88.9	11	23	ABB76233	
40	88.9	12	18	AAW36881	
40	88.9	12	22	ABP17219	

ALIGNMENTS

RESULT 1 ABP12751

HIV A02 super motif gag peptide #222.

15-JUL-2002 (first entry)

ABP12751;

ABP12751 standard; Peptide; 9 AA

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Sette A,
Baker DM,
                                                                                                                                                                                                                          HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.
Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1 -
                                   WPI; 2001-354887/37.
                                                                                        (EPIM-) EPIMMUNE INC.
                                                                                                              05-OCT-1999;
                                                                                                                                    05-OCT-2000; 2000WO-US27766
                                                                                                                                                           12-APR-2001.
                                                                                                                                                                                WO200124810-A1.
                                                                                                                                                                                                     Human immunodeficiency virus type 1.
                                                       Sidney J,
Celis E,
                                                                                                              99US-0412863.
                                                        Southwood S, Livingston BD, Kubo RT, Grey HM;
                                                                  Chesnut
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RESULT 2
ABP17961
ID ABP7
XX ABP1
XX ABP1
XX ABP1
XX ABP1
XX HIV
XX YUU
XX YUU
XX HUM
XX ANT:

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                              Claim 32; Page 237; 448pp; English
                                                                                  Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HIV: HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
antigen; vaccine; HIV infection; immunisation; virucide.
                                                                                                                                                                                                                                         Baker
                                                                                                                                                                                                                                                                                                                                                                                        05-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                               05-OCT-2000; 2000WO-US27766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HIV B58 super motif gag peptide #180
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                                                                                                                                                                                                                                                                                                                              (EPIM-) EPIMMUNE INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention
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                                                                                                                                                                                2001-354887/37.
                                                                                                                                                                                                                                      ₽,Þ
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9; Conserv
                                                                                                                                                                                                                                      Sidney J,
Celis E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ø
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                                                                                                                                                                                                                                   Southwood S, Livingston BD, Kubo RT, Grey HM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       describes a composition (I) comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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Pred. No.
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                                                                                                                                                                                                                                                                     Chesnut
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RESULT 3
ABB80017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC The present invention describes a composition (I) comprising a prepared CC human immunodeficiency virus-1 (HIV-I) group comprising an amino acid CC sequence selected from 51 defined amino acid sequences (ABL25347 to CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) CC may be used for immunising subjects against HIV-I infections. The use of CC group-based vaccines has several advantages over traditional vaccines, CC particularly when compared to the use of whole antigens in vaccine CC antigens is directed largely toward variable regions of the antigen, CC allowing for immune escape due to mutations. The groups for inclusion in a group-based vaccine may be selected from conserved regions of viral or CC tumour-associated antigens, which therefore reduces the likelihood of CC escape mutants. Furthermore, immunosuppressive groups that may be present CC in whole antigens can be avoided with the use of group-based vaccines. CC and additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the CC composition of the groups, achieving, for example, enhanced composition for the target disease. Similar engineering of the response can be modulated, as continuogenicity. Accordingly, the immune response can be modulated, as continuogenicity. Accordingly, the immune response can be modulated, as continuogenicity and traditional approaches. ABP11501 to ABP25412 convention.
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                               Cathepsin S; antiallergic; antiasthmatic; dermatological; pyrazole; atopic allergy; hay fever; asthma; atopic dermatitis; food allergy; allergy; dust; pollen; mold; pet dander; pet hair.
                                                                                                                                                                              06-SEP-2000; 2000US-230407P.
10-AUG-2001; 2001US-0927324.
                                                                                                                                                                                                                                                                                                                                                Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cathepsin S inhibition assay substrate peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB80017 standard; peptide; 10
                                              WPI; 2002-393814/42.
                                                                            Karlsson L, Khatuya H,
Tays KL, Thurmond RL,
                                                                                                               Butler CR,
                                                                                                                                                                                                                                 05-SEP-2001; 2001WO-US27429
                                                                                                                                                                                                                                                                  14-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB80017;
                                                                                                                                             (ORTH ) ORTHO-MCNEIL PHARM INC
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9; Conserv
                                                                            Cai H, Edwards JP,
, Khatuya H, Meduna
Thurmond RL, Wei J;
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100.0%;
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Pred. No.
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SP, Pio BA,
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7.8e+05;
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on CA, S
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Treatment of allergic conditions e.g. atopic dermatitis or asthma comprises administration of pyrazole derivative that inhibits cathepsin

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Best Local :
                                                                                                                                                                                                                                                                          New purified luciferase polypeptide, useful for identifying protease activity modulators, comprises recognition site cleavable by protease, where cleavage of polypeptide results in decreased luciferase activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the treatment of allergic conditions including atopic allergies, e.g. hay fever, asthma, atopic dermatitis, food allergies and allergies to dust, pollen, mold, pet dander or pet hair. The current sequence represents a cathepsin S inhibition assay substrate peptide.
           The invention relates to a purified polypeptide having luciferase activity and a recognition site specifically cleavable by a protease, where cleavage results in a decrease in luciferase activity. The polypeptide comprises a localisation sequence which is linked to the luciferase polypeptide by the cleavable recognition sequence. The polypeptide is useful for identifying a protease (Caspase-3) activity modulator, an inhibitor of apoptosis and for detecting luciferase activity in a sample. The polypeptide is used for characterising and identifying cellular processes associated with metabolism, cell growth and cell death e.g. apoptosis and for measuring protease activity. The protease measurement methods are useful for characterising, identifying cellular blochemical pathways as well as identifying diagnostic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to the treatment of allergic conditions, comprisi the administration of a pyrazole derivative. The activity of derivative of the invention may be described as, antiallergic, antiasthmatic and dermatological. They act as cathepsin S inhibitors and may be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE19118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE19118 standard;
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                                                                                                                                                                                                                                Claim 63; Page
                                                                                                                                                                                                                                                                                                                                                WPI; 2002-195809/25
                                                                                                                                                                                                                                                                                                                                                                                                             (CHEM-) CHEMICON INT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell death.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Luciferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protease peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAY-2002 (first entry)
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nes 9; Conserv
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for modulating diseases or disorders associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              enzyme;
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                                                                                                                                                                                                                                24;
                                                                                                                                                                                                                           56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protease; cell growth; apoptosis; therapeutic;
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100.0%;
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Pred. No.
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0.13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         derivatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        comprising
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    biochemical pathways. The polypeptide is also useful as a substratus study agents or conditions that cleave the recognition site and for determining amount of protease in a sample and for monitoring the activity of protease inside a cell that expresses a recombinant luciforase. The present sequence is a protease peptide used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                      Gag protein; antiviral; nucleic
protease recognition site; PRS;
                                                                                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus Gag protein protease cleavage sequence
                                                                                                                                                                                                                                                                                                                                                                                                                08-MAY-2002
                                                                                                                                                                                                                                                                                            WO200210430-A2
                                                                                                                                                                                                                                                                                                                     Cleavage-site
                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus type
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU75795
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU75795 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 KARVLAEAM 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KARVLAEAM 9
                                                                                                                                                                                                                                                                                                                                                              immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 9; Conserv
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                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                            /label= HIV_protease_cleavage_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
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                                                                                                                                                                                                                                                                                                                                                                      PRS; viral drug
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                              acid construct; viral protease;
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0.13;
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                                                                                                                                                                                                                                                                                                                                                                     resistance; HIV;
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New nucleic acid construct for detecting anti-viral drugs, comprises polynucleotide cassette encoding a chimeric polypeptide with two polypeptide sequences and a protease recognition site cleavable by a virally encoded protease Example 1; Page 32; 93pp; English.

31-JUL-2000; 2000US-0629969. 30-JUL-2001; 2001WO-IL00702

(AMID-) AMIDUT

WPI; 2002-188753/24

07-FEB-2002.

nucleic acid construct of the invention is useful for uncovering molecules having antiviral activity or for determining viral drug resistance and the chimeric peptide is also useful for detecting the presence of a virus in a cell. Other uses of the invention are detecting viral encoded protease found in infected cells or detecting the presence or absence of viral infection. The nucleic acid construct is useful for phenotypic testing of human immunodeficiency virus (HIV) drug resistance for invention enables screening of molecules in an easy and rapid manner The present invention relates to a new nucleic acid construct that comprises a polynucleotide cassette encoding a chimeric polypeptide. The chimeric polypeptide comprises a first polypeptide sequence, a second polypeptide sequence translationally fused to the first sequence, and a protease recognition site (PRS) cleavable by a virally encoded protease, where cleavage of the PRS leads to a detectable signal. The

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RESULT 6
ABP17190
ID ABP17190
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cc human immunodeficiency virus-1 (HTV-1) group comprising an amino acid composition of the sequence selected from 51 defined amino acid sequences (ABLZ3347 to CABPZ3397). (I) has virucide activity and can be used in vaccines. (I) CC may be used for immunising subjects against HTV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, CC particularly when compared to the use of whole antigens in vaccine CC compositions. There is evidence that the immune response to whole CC antigens is directed largely toward variable regions of the antigen, CC allowing for immune escape due to mutations. The groups for inclusion in CC an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of CC escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines.

CC An additional advantage of an group-based vaccine approach is the ability the
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Best Local
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Baker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu; v1f; tat; cytotoxic T lymphocyte; CTL; immune response; epito antigen; vaccine; HIV infection; immunisation; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP17190 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 KARVLAEAM 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention describes a composition (I) comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-354887/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KARVLAEAM 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ŗ,Þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32;
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9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPIMMUNE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           groups, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sidney J,
Celis E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        that were used in the invention for HIV detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       221;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              448pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gag peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        comprising human immunodeficiency if for vaccinating against HIV-1 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Southwood S, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
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Pred. No
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Livingston BD,
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.13;
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                            The invention relates to a method of treating allergic conditions comprising administration of a composition comprising a substituted pyrazole (I) or a salt, amide or entering method is used for treating allergic conditions, e.g. hay fever, asthma, atopic dermatitis and food allergies. The present sequence represents human cathepsin S substrate peptide used in an assay to demonstrate the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP11501 to ABP25412 represent peptide sequences used in the exemplification of the present
                                                                                                                                   Treating allergic conditions, and food allergies, comprises
                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                         06-SEP-2000;
10-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                     Example 37; Page 92; 115pp; English
                                                                                                                                                                                        Thurmond
                                                                                                                                                                                                  Cai H,
                                                                                                                                                                                                                    (ORTH ) ORTHO-MCNEIL PHARM INC
                                                                                                                                                                                                                                                                          05-SEP-2001;
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                                                                                                                                                                                                                                                                                                                                                Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                    Key
                                                                                                                                                                                                                                                                                                                                                                                                                                             food
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                                                                                                                                                                   2002-527344/56
                                                                                                                                                                                                                                                                                                                                                                                                                                             allergy
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                                                                                                                                                                                       Edwards JP
d RL, Wei
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9; Conser
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2001US-0927188
                                                                                                                                                                                                                                                                                                                                                                                                                                                       allergy; pyrazole; hay fever; asthma; atopic dermatitis;
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                                                                                                                                                                                  4 JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S substrate
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                                                                                                                                                                                                                                                                                                                                       /label= C-terminal
                                                                                                                                                                                                                                                                                                                                                           /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entry)
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                                                                                                                                                                                                                                                                                                                                                                                "Aedens-Glu"
                                                                                                                                                                                                                                                                                                                                                          "Dabcyl"
                                                                                                                                                                                                Karlsson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide
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Pred.
                                                                                                                                   e.g. hay fever, asthma, atopic dermatitis administration of a substituted pyrazole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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No.
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0.15;
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Length 11

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RESULT 8
ABB76233
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Best Local Similarity
"heres 9; Conserv
                                                                                             The present sequence is a peptide used as substrate for a cathepsin S inhibition assay. The Km for the substrate is around to sum but the presence of substrate inhibition makes kinetic analysis difficult. With 20 uM substrate, the assay rate is linear over the range of 1-8 ng cathepsin S in 100 ul reaction. Using 2 ng/well of cathepsin S, the production of product is linear and yields about 7-fold signal after 20 min with only 20% loss of substrate. Primary assays are run by quenching the reaction after 20 min and then measuring the fluorescence. For other assays, measurements are taken every min for 20 min. The rate is calculated from the slope of the increase and the percent inhibition is calculated from this. The present invention relates to the use of cathepsin S inhibitors to treat an allergic condition, especially an atopic IgE-mediated allergic condition such as hay fever, asthma, atopic dermatitis or a food allergy candidated. The later allerges may include dust, pollen, mould, and pet
    Query Match 88.9
Best Local Similarity 100
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cathepsin S; inhibitor; allergy; hay fever; asthma; food allerg atopic dermatitis; antiallergic; antiasthmatic; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB76233;
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                                                                                                                                                                                                                                                                                                                                                              Use of cathepsin S inhibitor for treating hay fever, asthma, atopic dermatitis or a
                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-443877/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gu Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-SEP-2000; 2000US-230407P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antiinflammatory; immunosuppressive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Substrate for cathepsin S inhibition assay.
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                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ORTH ) ORTHO-MCNEIL PHARM INC.
                                                                                                                                                                                                                                                                                                                                     Example 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
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                                                                                      암
                                                                                     pet
                                                                                                                                                                                                                                                                                                                                   Page
                                                           11 AA;
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                                                                                      hair.
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88.9%; but
100.0%; Pr/
0;
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                                                                                                                                                                                                                                                                                                                                   English.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Thurmond
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                  Score 40; DB 23;
Pred. No. 0.15;
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Pred. No.
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. 0.15;
                                                                                                                                                                                                                                                                                                                                                              an allergic condition, food allergy
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                             Length 11;
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ID ABP1
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Mismatches

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ABP17219 standard; Peptide; 12 AA

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RESULT 9
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                                                                               Query Match
                                                                                                                                                                of a ricin-like protein in a novel recombinant protein. A nucleic acid (see AAT97900) encoding such a construct is obtained by PCR mutagenesis of the wild-type ricin linker sequence. The invention provides novel recombinant proteins which incorporate the A and B chains of a ricin-like toxin (preferably the A and B chains of ricin) linked by a heterologous linker sequence containing a cleavage recognition site for a retroyiral protease such as HIV protease (see AAM36880-82), HTLV-I (see AAM36883-43) or HTLV-II (see AAW36885-65). The recombinant proteins selectively inhibit or destroy mammalian cells infected with a retroyirus such as cancer cells associated with HTLV or cells associated with HTLV. The recombinant proteins are non-toxic until the ricin A chain is liberated from the B chain by a retroyiral protease, and thus can
                                                                                                                                                                                                                                                                                                                                                                                                                                 DNAs encoding ricin like toxins A and B - are linked of containing cleavage site for retroviral protease, used destroy mammalian cells infected with retrovirus
                                                                                                                                                                                                                                                                                                                                               protease.
of a rici
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
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                                                                                                             Sequence
                                                                                                                                                        be used
                                                                                                                                                                                                                                                                                                                                                                           This claimed
                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Page 41; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Borgford T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CANG-) CANGENE CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-APR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AIDS; infection; therapy; linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ricin; toxin; antiviral; virucide; retrovirus; protease; HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIV protease cleavage recognition site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                       Local Similarity
nes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               μ
2 KARVLAEAM 10
                      2 KARVLAEAM 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EKARVLAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1997-549735/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EKARVLAEA
                                                                                                                                         cell
                                                                                                                                        to specifically target infected ell binding component.
                                                                                                             12 AA;
                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                           peptide is a cleavage recognition site for a HIV is utilised as a linker between the A and B chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96US-0016509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97WO-CA00288
                                                     88.9%; Score 40;
100.0%; Pred. No.
Live 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12
                                                       Mismatches
                                                                   DB 18;
0.16;
                                                                                                                                                        ral protease, and thus can cells without the need
                                                                                                                                                                                                                                                                                                                                                                                                                                                are linked via linker
otease, used to inhibit or
                                                       0;
                                                                                  Length 12;
                                                       0
                                                     Gaps
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RESULT 11
ABP17220
ID ABP17
XX
AC ABP17
XX
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                                                                                                                                                                                                                                                                                                               The present invention describes a composition (1) comprising a prepared CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid Sequences (ABL25347 to CC ABP25397). (1) has virucide activity and can be used in vaccines. (1) CC may be used for immunising subjects against HIV-1 infections. The use of Group-based vaccines has several advantages over traditional vaccines, CC particularly when compared to the use of whole antigens in vaccines. CC compositions. There is evidence that the immune response to whole compositions is directed largely toward variable regions of the antigen, CC allowing for immune escape due to mutations. The groups for inclusion in a group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of CC escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the CC composition of the groups, achieving, for example, enhanced composition of the target disease. Similar regionesing the response can be possible with traditional approaches. ABP11501 to ABP25412 crepresent peptide sequences used in the exemplification of the present convention.
                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                       Query Match
Best Local :
                 ABP17220
                                                 ABP17220 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu; v1f; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1 -
                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 32; Page 221; 448pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-354887/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Baker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-OCT-2000; 2000WO-US27766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200124810-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (EPIM-) EPIMMUNE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HIV B27 super motif gag peptide #95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP17219;
                                                                                                                                    2 KARVLAEAM 10
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4 KARVLAEAM 12
                                                                                                                                                                                                       Local Similarity
nes 9; Conserv
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Celis E,
                                                                                                                                                                                                                                                                        12
                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                        ξ
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                                                 Peptide; 12 AA.
                                                                                                                                                                                                                       88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Southwood S, Livingston BD, Kubo RT, Grey HM;
                                                                                                                                                                                                     0
                                                                                                                                                                                                                       Score 40;
Pred. No.
                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                     DB 22;
0.16;
                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                   Length 12;
                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chesnut R;
                                                                                                                                                                                                     0;
                                                                                                                                                                                                   Gaps
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AAR25633
ID AAR2
XX
AC AAR2
XX
DT 17-E
DT 19-J
XX
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                            RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a composition (I) comprising a prepared CC human immunodeficiency virus-I (HIV-I) group comprising an amino acid Sequence selected from 51 defined amino acid sequences (ABL25347 to CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) CC may be used for immunising subjects against HIV-I infections. The use of CC group-based vaccines has several advantages over traditional vaccines, CC particularly when compared to the use of whole antigens in vaccine CC compositions. There is evidence that the immune response to whole CC antigens is directed largely toward variable regions of the antigen, CC allowing for immune escape due to mutations. The groups for inclusion in CC an group-based vaccine may be selected from conserved regions of viral or CC tumour-associated antigens, which therefore reduces the likelihood of CC escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. CC An additional advantage of an group-based vaccine approach is the ability CC composition of the groups (CTL and HTL), and further, to modify the CC composition of the groups, achieving, for example, enhanced CC immunogenicity. Accordingly, the immune response can be modulated, as a properiate, for the target disease. Similar engineering of the response CC is not possible with traditional approaches. ABP11501 to ABP35412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sette A,
Baker DM,
                                                                      AAR25633;
                                                                                                      AAR25633 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.
                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 32; Page 221; 448pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-354887/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-OCT-2000; 2000WO-US27766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HIV B27 super motif gag peptide #96.
                                                                                                                                                                                                                                                                                                                                                                                                represent peptide sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EPIM-) EPIMMUNE INC
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                                                                                                                                                                                                 4 KARVLAEAM 12
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Celis E,
                                                                                                                                                                                                                                                                                                                                            12 AA
                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9905-0412863
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                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                         88.98;
                                                                                                         14 AA
                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                      Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S, Livingston Grey HM;
                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                    DB 22
0.16;
                                                                                                                                                                                                                                                                                                       22;
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                                                                                                                                                                                                                                                                                                     Length 12
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17-DEC-2001 19-JAN-1993

(updated)
(first entry)

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RESULT 13
AAR68705
ID AAR68
XX AAR68
XX O7-SE
DT 07-SE
XX T-Cel
XX GP160
XX UP160
XX
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequences given in AAR25632-38 are peptides which are hydrolysed by aspartyl proteinase (AP) in the assay of the invention. These peptides have labelled C-terminal portions which are polar. These portions are separated from the unlabelled hydrophobic N-terminal portions by hydrolysis by AP. Following hydrolysis of these peptides with AP, the hydrolysed polar portion is separated from the unhydrolysed polar portion is separated from the unhydrolysed polar portion of a period to the amount of hydrolysed polar portide determined. This assay can be used to detect inhibitors of AP with potential as therapeutic agents, eg. for treating AIDS. This assay has a higher separated the polar period of the period
                                                                                                                                                                                                                   T-cell; epitope; gp160; gag; pol;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sensitivity than previous methods.

(Note: Revised entry submitted to correct the patent number format of US Government-owned NTIS applications to prevent clashes with ongoing US granted patent numbers. For further information please visit the Derwent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Assay for retroviral aspartyl proteinase - provides rapid accurate and inexpensive method for detecting aspartyl proteinase inhibitors, e.g. for AIDS treatment
                                                                                                                                                                                                                                                                                                                             T cell epitope, P24M.
                                                                                                                                                                                                                                                                                                                                                                                                         07-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR68705;
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                                                                                                                                               Human immunodeficiency virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (USSH ) US DEPT HEALTH & HUMAN SERVICE.
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   22-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 KARVLAEAM 11
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9; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                               HIV-1; core protein; p24E; B-cell;
vaccine; multimeric peptide; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hydrolisation; inhibitor; therapeutic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88.9%;
100.0%
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Pred. No.
                                                                                                                                               type 1.
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0.19;
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                                                                                                                                                                                                                   antigen;
3D organisation.
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RESULT 14
AAW25875
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents the T-cell epitope, P24M, which may be linked to a B-cell epitope from the V3 (MN) loop from HIV-1. These chimeric peptides may then be used in the production of HIV-1 vaccines. These peptide sequences may also be used in the production of multimeric peptides in which the linear peptides are C-terminally modified by the addition of a Lys residue which is modified on its epsilon amino acid to carry an additional copy of the peptide molecule. The linear and multimeric peptides may be used for the treatment of AIDS by acting to displace the binding of HIV virus to human or animal cells or by disturbing the 3D organisation of the virus.
                                                              WPI;
                                                                                                                                                                                                                                                                                                           HIV T-helper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel tandem synthetic HIV-1 peptide(s) - comprising T-cel epitope of gag protein linked to B-cell epitope of V3 loop protein of an HIV-I isolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chong P,
Claim 1; Column 73; 41pp; English
                         Tandem synthetic HIV peptide(s) useful as immunogens - comprising gag protein T-cell epitope linked to env protein B-cell epitope
                                                                                                              (CONN-) CONNAUGHT LAB LTD
                                                                                                                                      09-JUN-1994;
09-JUN-1993;
                                                                                                                                                                           09-JUN-1993;
                                                                                                                                                                                                  17-JUN-1997
                                                                                                                                                                                                                         US5639854-A.
                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                       HIV; human immunodeficiency virus; gag; T-cell; B-cell; epitope; env; V3 loop; vaccine; determinant; chimaeric.
                                                                                                                                                                                                                                                                                                                                      22-OCT-1997
                                                                                                                                                                                                                                                                                                                                                              AAW25875
                                                                                                                                                                                                                                                                                                                                                                                    AAW25875 standard; peptide; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
9; Conser
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                                                                                    Klein MH,
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                                                                                                                                                                                                                                                                                                           determinant core peptide p24M
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                                                                                                                                     94US-0257528
93US-0073378
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Pred. No.
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0.2;
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Best Local Similarity
Matches 9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-JUN-1994;
09-JUN-1993;
05-JUN-1995;
                                                                   The invention relates to a novel immunogenic composition for use in vaccines for the treatment of HIV-1 comprising an HIV-1-derived T-cell epitope linked to an HIV-1-derived B-cell epitope. The T-cell epitopes are generally designed based on the p24 core protein and the B-cell epitopes from the V3 loop of the gp120 protein from various HIV-1 strains. This peptide is a T-cell epitope derived from the HIV-1 strain
     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                            Chong P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to new synthetic peptides comprising at least one mains acid sequence comprising an HIV gag protein T-cell epitope linked at its C- or N-terminus to an amino acid sequence comprising a B-cell epitope of the V3 loop of an HIV env protein, which can be used to generate vaccines against HIV-1. The T-cell epitope sequence is pref. selected from the T-helper determinant core peptides P24E, P24E
                                                                                                                                                                                                                                              Disclosure; Column 23-24; 40pp; English.
                                                                                                                                                                                                                                                                                                               Synthetic human immunodeficiency virus-1 peptide(s) - containing T-cell epitope and B-cell epitope(s) are candidate vaccines against
                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-556461/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US5817754-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus type 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CONN-) CONNAUGHT LAB LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     V3 loop.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunogen; vaccine; HIV-1; T-cell; B-cell; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                w
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                                               core protein.
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93US-0073378.
95US-0464329.
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Pred. No.
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0.2;
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Query Match Best Local Similarity

88.9%; 100.0%;

Score 40; Pred. No.

DB 19;

Length 15;

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Matches 9; Conservative 0; Mismatches 0;

Qy 2 KARVLAEAM 10
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Db 3 KARVLAEAM 11
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Indels

0;

Gaps

0

Search completed: March 13, 2003, 18:49:14 Job time : 26.5455 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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219
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seq length:
  444444444
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                                                                                                                                                                                                                                                                                                                                                                      Issued_Patents_AA:*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*
  EKARVLAEAM 10
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                 US-09-147-208-21
US-08-460-602A-76
US-08-463-966A-76
US-08-463-966A-76
US-08-464-329A-76
US-08-464-329A-76
US-08-463-966A-47
US-08-463-966A-47
US-08-463-966A-47
US-08-463-968A-47
US-08-463-968A-47
US-08-463-329A-47
US-08-463-328A-77
US-08-463-396A-78
US-08-463-396A-78
US-08-463-396A-78
US-08-463-396A-78
US-08-463-396A-78
US-08-463-396A-78
US-08-463-396A-78
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US-09-053-941-15
US-09-817-413-15
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88.9	88.9			88.9						88.9		88.97	88.9	88.9	88.9	88.9	88.9	
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US-09-370-368-3	US-09-621-625A-17	US-09-621-625A-2	US-08-987-867A-4	US-08-389-459A-4	US-08-444-882-4	US-08-589-446-4	US-09-621-625A-25	PCT-US93-02142-6	US-08-477-081-6	US-08-117-981-6	US-09-117-217-8	US-09-621-625A-27	US-08-467-881A-78	US-08-467-881A-77	US-08-462-507A-78	US-08-462-507A-77	US-08-464-329A-78	
Sequence 3, Appli	Sequence 17, Appl	Sequence 2, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 25, Appl	Sequence 6, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 8, Appli	Sequence 27, Appl	Sequence 78, Appl	Sequence 77, Appl	Sequence 78, Appl	Sequence 77, Appl	Sequence 78, Appl	

ALIGNMENTS

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SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
i Type: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-792-553-4
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                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DATA:
COMPUTER: PATENTIA RELEASE #1.0, Ver
SOFTWARE: PATENTIA RELEASE #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION UNUBER: US/08/792,553
FILING DATE: 31-JAN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07257/04100
TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 4:
INFORMATION FOR SEQ ID NO: 4:
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US-08-792-553-4
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Patent No. 5981200
GENERAL INFORMATION:
APPLICANT: Tsien, Roger Y.
APPLICANT: Heim, Roger
                                                              Query Match
Best Local s
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 4422
CITY: La Jolla
CTATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SECULIARIES CORRESPONDENCE ADDRESS:

***CORRESPONDENCE FISH & RICHARDSON P.C.

***CORRESPONDENCE FISH & RICHARDSON P.C.

***CORRESPONDENCE FISH & RICHARDSON P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                 2 KARVLAEAM 10
1 KARVLAEAM 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92037
                                                               Similarity
9; Conserv
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Heim, Roger
ENTION: Tandem Fluorescent Protein Constructs
                                                                   Conservative
                                                          88.9%; 5cc
100.0%; Pr
                                                                                 Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                        07257/041001/UC 96-160-2
                                                                   Mismatches
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                                                                                 DB 2;
0.033;
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                                                               Gaps
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US-09-053-941-15

Sequence 15, Apple Sequence 15,

Application US/09053941

GENERAL INFORMATION:

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RESULT 4
US-09-147-208-21
; Sequence 21, Application US/09147208
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                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
PUBLICATION INFORMATION:
JOURNAL: Meth. Enzymol.
VOLUME: 38
PAGES: 299-
DATE: 1974
US-09-817-413-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Human immunodeficiency virus type 1
PUBLICATION INFORMATION:
JOURNAL: Meth. Enzymol.
VOLUME: 38
PAGES: 299
DATE: 1974
US-09-053-941-15
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APPLICANT: KOPROWSKI, HILARY
APPLICANT: KOPROWSKI, HILARY
ITILE OF INVENTION: CHIMERIC VIRAL PROTEINS
FILE REFERENCE: Chimeric Viral Proteins
CURRENT APPLICATION NUMBER: US/09/053,941
CURRENT FILING DATE: 1998-04-02
EARLIER APPLICATION NUMBER: 60/043,380
EARLIER APPLICATION NUMBER: 60/043,380
EARLIER FILING DATE: 1999-04-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
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Matches
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SOFTWARE: Patentin Ver. SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/817,413
CURRENT FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: 60/043,380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: SRINIVISAN, ALGARSAMY
APPLICANT: KOPROWSKI, HILARY
TITLE OF INVENTION: CHIMERIC VIRAL PROTEINS
FILE REFERENCE: Chimeric Viral Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1999-04-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 10
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                           ENGTH: 10
                                                                                                                                                        Local Similarity 100 nes 9; Conservative
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                                                                                        KARVLAEAM 9
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-147-208-21
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Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                      Patent No. 5639854
GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 76,
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                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/257,528B
FILING DATE: 09-JUN-1994
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INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
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REGISTION NUMBER: 38,003
REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
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FILING DATE: 02-MAR-1999
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Rudolph, John R.
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS: ADDRESSE: BERESKIN & PARR
CLASSIFICATION:
ATTORNEY/AGENT IN
                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                               STREET: Suite CITY: Toronto
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                                                                                                                                                                                                                  STATE:
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CITY: Toronto
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ZIP: M5H 3Y2
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Suite 701, 330 University Avenue
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 INFORMATION:
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100.0%; Pred. No.
Live 0; Mismatc
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                                                                                        Version #1.25
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Query Match
Best Local Similarity
Thehes 9; Conserv
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US-08-460-602A-76
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Patent No. 5759769
          Query Match
                                                                                                                                                                                                                                                  TELEFAX: (416) 595-116:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TYPE: amino acid
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APPLICATION NUMBER: 08/07:
APPLICATION NUMBER: 09-JUN-1993
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
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LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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REFERENCE/DOCKET NUMBER: 10
REFERENCE/DOCKET NUMBER: 10
REFERENCE/DOCKET NUMBER: 11
REFERENCE/DOCKET NUMBER: 10
REFERENCE/DOCKET NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10,973
REFERENCE/DOCKET NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10,973
REFERENCE/DOCKET N
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                                                                                                                                                                                                             STRANDEDNESS:
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M5G 1R7
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KLEIN, Michel H.
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          Score 40;
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Length 15;
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                                            ; Sequence 7:
; Patent No.
                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                          US-08-465-217A-76
                                                                                        RESULT 8
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                                GENERAL
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                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/OCKET NUMBER: 1038-487 MIS:jb
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
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APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
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APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
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APPLICANT: SIA, Charles APPLICANT: CHONG, Pele
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                                                                                                                                   2 KARVLAEAM 10
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3 KARVLAEAM 11
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                             INFORMATION:
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amino acid
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                                                          Application US/08465217A
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             SIA, Charles D.Y.
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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CURRENT APPLICATION DATA:

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; STRANDEDNESS: sir
; TOPOLOGY: linear
US-08-465-217A-76
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CLASSIFICATION: 424
ATTORREY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
(416) 595-1155
                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: SIA, C
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NFORMATION FOR SEQ ID NO:
                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
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                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LENGTH: 15 amino acid
                                                                                                                                                                                                           TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides NUMBER OF SEQUENCES: 101
                                                                                                                                                                                                                                              APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
                                                                                                                                                                                                                                                                APPLICANT:
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PRIOR APPLICATION DATA:
08/073,378
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APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: Tandem
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
                                                                                                                                     STREET: Suite
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 9; Conserv
                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                      COUNTRY:
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FILING DATE: 09-JUN-1993
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OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: M5G 1R7
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CITY: Toronto
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M5G 1R7
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PatentIn Release #1.0, Version #1.25
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100.0%; Pred. No.
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RESULT 10
US-08-462-507A-76
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TOPOLOGY:
US-08-464-329A-76
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CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528

FILING DATE: 09-JUN-1994

CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378

TITING DATE: 09-JUN-1993
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                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 101
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LENGTH: 15 amino acids
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APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
                            ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: Sim & McBurney
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REFERENCE/DOCKET NUMBER: 1038-449 MIS:jb
TELECOMMUNICATION INFORMATION:
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APPLICANT: KLEIN, Michel H.
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                          APPLICATION NUMBER: US/08/462,507A FILING DATE: 05-JUN-1995
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STATE: Ontario
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STRANDEDNESS: sir
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SYSTEM: PC-DOS/MS-DOS
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MICHAEL I.
MBER: 24,973
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Pred. No.
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                                    Query Match
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      Matches
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LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (416) 595-11 INFORMATION FOR SEQ ID NO:
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                                                                                                                          TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073
FILING DATE: 09-JUN-1993
                                                                                                                                                                                                   REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,881A
FILING DATE: 06-JUN-1995
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MEDIUM TYPE: Floppy
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APPLICANT: KLEIN, Michel H.
                                                                                                                                                                                                                                                               CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
      Local Similarity 100 hes 9; Conservative
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ZIP: M5G 1R7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Toronto
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les 9; Conserv
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                                                                                             TYPE: amino acid
STRANDEDNESS: sin
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                                                                                  OPOLOGY:
                                                                                                                                                                                                                                                 STEWART, MICHAEL
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Suite 701, 330 Un
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                   Score 40;
Pred. No.
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Pred. No. 0.05;
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                    DB 2;
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                                                                                                                                                                                                                                                    RESULT 13
                                                                                                                                                                                   Sequence 47, Application US/08460602A Patent No. 5759769
GENERAL INFORMATION:
                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                          APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                        APPLICANT: SIA, Charles D.Y.
                                               CITY: Toronto
                                                                 STREET:
                    COUNTRY:
                                                                               ADDRESSEE:
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Ontario Canada

Suite 701,

330 University Avenue

Sim & McBurney

101

Tandem Synthetic HIV-1 Peptides

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Query Match
Best Local Similarity
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                                                                                                                                                                                                            TELEFAX: (416) 595-11 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                            JUNO:

JACUTERISTICS:

32 amino acids

JACUTERISTICS:

32 amino acid

STRANDEDNESS:

TOPOLOGY:

157-5287
                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (416) 595-1155
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                                                                                                                                                                                                                                                                                     NAME: STEWART, MICHAEL REGISTRATION NUMBER: 24
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CITY: Toronto
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3 KARVLAEAM 11
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M5G 1R7
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5639854
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KLEIN, Michel H.
                                                        Conservative
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                                                      88.9%; Score 40;
100.0%; Pred. No.
tive 0; Mismatc
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                                                          Mismatches
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0.11;
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US-08-460-602A-47
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Best Local Similarity
Matches 9; Conserv
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                  APPLICATION NUMBER: US/08/463, FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
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TITLE OF INVENTION: Tandém Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEPAX. .....
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CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
08/257,528
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MEDIUM TYPE: Floppy disk
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CITY: Toronto
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                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                           COUNTRY:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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KLEIN, Michel H.
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100.0%;
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08/073,378
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Pred. No.
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US-08-465-217A-47
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Patent No. 5
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: 08/073,378
FILING DATE: 09-JUN-1993
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                                                                  INFORMATION FOR SEQ ID NO:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                             REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I
                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy
                                                 SEQUENCE CHARACTERISTICS:
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NAME: STEWART, MICHAEL I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/465,217A FILING DATE: 05-JUN-1995
   TYPE: amino acid STRANDEDNESS: si
                                                                                              TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Ontario
                   TYPE:
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                                 ENGTH:
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M5G 1R7
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amino acid
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KLEIN, Michel H.
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single
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Pred. No.
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Best Local Similarity 100.0%; Pred. No. 0.11;
Best Local Similarity 200.0%; Pred. No. 0.11;
Batches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2 KARULARM 10
Db 3 KARULARM 11
Search completed March 13, 2003, 18:53:52
Job time : 8.90909 secs 3, 18:53:52
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Minimum
Maximum
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Maximum Match
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        111111111 9876544
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seq length: 2000000000
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      us-10-050-200-7
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//cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
//cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
//cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
//cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
//cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
//cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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US-09-864-761-33475
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0 US-09-864-761-33475
0 US-09-861-574-48
0 US-09-815-242-11532
0 US-09-815-242-11532
0 US-09-815-242-11532
0 US-09-815-242-11532
US-09-916-497-59
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0 US-09-949-626-819
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                                     Sequence 1127, App Sequence 988, App Sequence 988, App Sequence 1932, App Sequence 93, Appl Sequence 344, App Sequence 344, App Sequence 11532, A Sequence 11819, App Sequence 1819, App Seq
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US-09-764-864-1127
; Sequence 1127, Application US/09764864
; Patent No. US20020132753A1
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US-09-861-270-2	US-09-880-505-125	US-10-051-643-125	US-09-898-461-7	US-09-815-242-12876	US-09-815-242-12539	US-09-815-242-5617	US-09-925-297-534	US-09-864-761-35465	US-09-864-761-36003	US-10-016-993-3	US-09-824-178-4	us-10-016-993-4	US-09-824-178-3	US-09-824-178-12	US-10-099-766-12	US-09-815-242-10903	US-09-925-301-1335	US-10-054-295-54	US-10-054-295-8	US-10-053-758-54	US-10-053-758-8	US-09-438-486-54	US-09-438-486-8	US-09-766-253-54	US-09-766-253-8
Sequence 2, Appli	Sequence 125, App	Sequence 125, App	Sequence 7, Appli	Sequence 12876, A	Sequence 12539, A	Sequence 5617, Ap	Sequence 534, App	Sequence 35465, A	Sequence 36003, A	Sequence 3, Appli	Sequence 4, Appli	ځ.	Sequence 3, Appli	Sequence 12, Appl	Sequence 12, Appl	Sequence 10903, A	Sequence 1335, Ap	Sequence 54, Appl	Sequence 8, Appli	Sequence 54, Appl	Sequence 8, Appli	Sequence 54, Appl	Sequence 8, Appli	54,	Sequence 8, Appli

ALIGNMENTS

and Antibodies

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RESULT 2
US-10-101-464A-787
; Sequence 787, Application US/10101464A
; Publication No. US20030046728A1
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Higgins, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: SITE
; LOCATION: (124)
; OTHER INFORMATION:
US-09-764-864-1127
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Best Local Similarity
Watches 8; Conserv:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic acids, Proteins,
FILE REFERENCE: PTZ23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prior application data removed - consult PALM NUMBER OF SEQ ID NOS: 1792 SOFTWARE: PatentIn Ver. 2.0
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CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 14
TYPE: PRT
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CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR APPLICATION NUMBER: FCT/US00/00724
PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR FILING DATE: 2000-01-11
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Best Local Similarity burnershes B; Conservative
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 787
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SEQ ID NO 988
LENGTH: 909
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LOCATION: (52)
OTHER INFORMATION: Y
NAME/KEY: SITE
NAME/KEY: (58)
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TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR EILING DATE: 2000-03-08
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NUMBER OF SEQ ID NOS: 1556
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                                                                                               LOCATION: (58)
OTHER INFORMATION:
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OTHER INFORMATION:
NAME/KEY: SITE
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LOCATION: (62)
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NAME/KEY: SITE
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196 AEQQNLKSQN 205
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Best Local S
Matches 7
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Patent No. US20020055627A1
GENERAL INFORMATION:
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SEQ ID NO 988
LENGTH: 909
             Query Match
Best Local
 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Nucleic Acids, Proteins FILE REFERENCE: PA102 CURRENT APPLICATION NUMBER: US/09/925,299 CURRENT FILING DATE: 2001-08-10
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OTHER INFORMATION: >
NAME/KEY: SITE
LOCATION: (851)
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NAME/KEY: SITE
LOCATION: (52)
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NAME/KEY: SITE
LOCATION: (32)
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EAVEQOKVKNNDL 672 ERAEQQRLKSQDL

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APPLICANT: MCNĀBb, ANDRIA

APPLICANT: MCNĀBb, ANDRIA

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.478C17

CURRENT APPLICATION NUMBER: US/09/902,941

CURRENT FILING DATE: 2001-07-10

NUMBER OF SEO ID NOS: 2002

SOFTWARE: FASTSEQ for Windows Version 4.0

SEO ID NO 1934

LENGTH: 464

TYPE: PRT

ORGANISM: Homo spaiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Watches 6; Conserv?
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; ORGANISM: Homo sapiens
US-09-902-941-1932
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CURRENT FILING DATE: 2001-07-10
NUMBER OF SEQ ID NOS: 2002
SOFTMARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1932
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                                                                                                                                                                                                                                                                                                                                              APPLICANT: Henderson, Robert A.
APPLICANT: Wang, Tongtong
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Johnson, Jeffrey C.
APPLICANT: Retter, Marc W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: MCNABB, AND TIALE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121,478C17
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APPLICANT:
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Fanger, Gary R.
Vedvick, Thomas S.
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McNabb, Andria
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McNabb, Andria
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Watanabe, Yoshihiro
Johnson, Jeffrey C.
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Carter, Darrick
Fanger, Gary R.
Vedvick, Thomas S.
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milarity 46.2%;
Conservative
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; SEQ ID NO 93
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo s
US-09-738-973-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; SOFTWARE: FastSEQ for Windows Version 3.0; SEQ ID NO 93; LENGTH: 162; TYPE: PRT; ORGANISM: Homo sapien US-09-854-133-93
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US-09-854-133-93
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Publication No.
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Best Local
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Best Local
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Query Match
Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT FILING DATE: 2001-05-11
                                                                                                             TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF FILE REFERENCE: 210121.475C9
CURRENT APPLICATION NUMBER: US/09/738,973
CURRENT FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 587
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 EEAEQKRLKT 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ERAEQQRLKS 10
                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
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7; Conserv
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                                                                                                                                                                                                              Mannion, Jane
Kalos, Michael D.
                                                                                                                                                                                                                                         Benson, Darin R.
Elliot, Mark
                                                                                                                                                                                                                                                                     Algate, Paul A.
Secrist, Heather
Indirias, Carol Yoseph
                                                                                                                                                                                                                                                                                                                                       Henderson, Robert A.
Lodes, Michael J.
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                                                                                                                                                                                                                                                                                                                                                                        Reed, Steven G.
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56.5%;
70.0%;
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Pred. No.
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Score
Pred.
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DB 10;
44;
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                                                                                                                                                                                     LUNG CANCER
              Length 162;
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APPLICANT: ROSEN et al.
TITLE OF INVENTION: 143 Human Secreted Proteins
FILE REFERENCE: PS500P1
CURRENT APPLICATION NUMBER: US/09/986,480
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: PCT/US00/12788
PRIOR FILING DATE: 2000-05-11
PRIOR FILING DATE: 1999-05-13
PRIOR FILING DATE: 1999-05-13
                                                                                                   CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/006664
PRIOR APPLICATION NUMBER: PCT/US01/006664
PRIOR APPLICATION NUMBER: PCT/US01/006664
PRIOR APPLICATION NUMBER: PCT/US01/006664
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Sequence 33475, Application US/09864761

: Patent No. US20020048763A1

: GENERAL INFORMATION:
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 344
LENGTH: 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 344, Application US/09986480 Publication No. US20030027999A1 GENERAL INFORMATION:
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: Acomica-x-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139 ERAEEQARKEQE 150
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nes 7; Conserv
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                      APPLICATION NUMBER: PCT/US01/00669 FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01/00665 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EEAEOKRLKT 77
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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; Sequence 18, Application US/09916790
; Patent No. US20020061573A1
; GENERAL INFORMATION:
                                                               ; OTHER INFORMATION: Consensus amino acid sequence US-09-916-790-18
                                                                                                                                                                                                                                                                                              APPLICANT: Meyers, Rachael
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Silos-Santiago, Immaculada
TITLE OF INVENTION: 18431 AND 32374, NOVEL HU
TITLE OF INVENTION: KINASE FAMILY MEMBERS AN
FILE REPERENCE: 381552002700
CURRENT APPLICATION NUMBER: US/09/916,790
CURRENT FILING DATE: 2001-07-27
CURRENT FILING DATE: 2001-07-27
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                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version SEQ ID NO 18
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/221,543 PRIOR FILING DATE: 2000-07-28
                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
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                                                                                                       ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                     LENGTH: 341
TYPE: PRT
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30 APPLICATION NUMBER: US 60/234,687 FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US01/00661 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 09/608,408 FILING DATE: 2000-06-30
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APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
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ED IN HART, SIGNAL = 1.2

ED IN BRAIN, SIGNAL = 1.2

ED IN ADULT LIVER, SIGNAL = 1.4

ED IN HELA, SIGNAL = 0.94

ED IN HELA, SIGNAL = 6.3

ED IN BONE MARROW, SIGNAL = 0.74

ED IN BYA74, SIGNAL = 4.1

AN HIT: BE295973.1, EVALUE 5.00e-83

OT HIT: P49910, EVALUE 7.00e-38
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  Score 35;
Pred. No.
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  DB 10;
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; ORGANISM: Mus musculus US-09-801-574-42
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                                                                                                                                                                                FILE REFERENCE: ELITAA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Wang, Peijing Jeremy
APPLICANT: Page, David C.
TITLE OF INVENTION: Reproduction-Specific Genes
FILE REFERENCE: 0399 2007-002
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                                                                                     PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
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CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: 60/187,518
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: 60/261,557
PRIOR APPLICATION NUMBER: 60/261,557
PRIOR FILING DATE: 2001-01-12
NUMBER OF SED ID NOS: 90
                                                                                                                                                                                                                                                                                                                 APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
                                                         PRIOR FILING DATE: 2000-12-22 PRIOR APPLICATION NUMBER: 60/269,308
                                       PRIOR FILING DATE: 2001-02-16
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nes 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Wall, Daniel
Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                        Carr, Grant
                                                                                                                                                                                                                                                                                                                                                                                                       Yamamoto, Robert T.
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   Windows Version 4.0
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Pred. No. 1.4e+02;
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US-09-919-497-59
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                                    ; ORGANISM: Homo sapiens US-09-736-457-1819
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US-09-736-457-1819
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GENERRAL INFORMATION:
APPLICANT: MUTTER, GEOTGE L.
APPLICANT: MUTTER, GEOTGE L.
TYPE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 11532
LENGTH: 529
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Query Match
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CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/221,735
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 100
                                                                                                                                          FILE REFERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
                                                                                                                                                                                               APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C15
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TYPE: PRT
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59 AEEMRMKSQE 68
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                                                                                                                             FastSEQ for Windows Version 3.0
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Lodes, Michael /
Fanger, Gary
                                                                                                                                                                                                                                                                                                        Carter, Darrick
Retter, Marc
                                                                                                                                                                                                                                                                                                                                                Vedvick, Tom
                                                                                                                                                                                                                                                                          Fan, Liqun
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Pred. No. 3.6e+02;
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Pred. No. 2.4e+02;
Score 34;
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DB
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Length 831;
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Matches Query Match SEQ ID NO 42

GENERAL

APPLICANT:

APPLICANT:

APPLICANT:

APPLICANT:

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Best Local Similarity 58.3%; Prod. No. 3.9e-02;
Matches 7; Connervative 2; Mismatches 3; Indels 0; Gaps 0;

Oy 2 RANDORLESOL 13

Db 25 MARNORDU 36

Search completed; March 13, 2003, 18:54:49

Job time: 12.1091 secs

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Maximum DB seq length: 2000000000
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         Published_Applications_AA:*

1: /cgn2_6/ptcdata/1/pubpaa/PCT_NEW_PUB.pep:*

2: /cgn2_6/ptcdata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptcdata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptcdata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptcdata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptcdata/1/pubpaa/US07_PUBCOMB.pep:*

7: /cgn2_6/ptcdata/1/pubpaa/US07_PUBCOMB.pep:*

8: /cgn2_6/ptcdata/1/pubpaa/US09_NEW_PUBCOMB.pep:*

9: /cgn2_6/ptcdata/1/pubpaa/US09_NEW_PUBCOMB.pep:*

10: /cgn2_6/ptcdata/1/pubpaa/US09_NEW_PUBCOMB.pep:*

11: /cgn2_6/ptcdata/1/pubpaa/US09_NEW_PUBCOMB.pep:*

12: /cgn2_6/ptcdata/1/pubpaa/US09_NEW_PUBCOMB.pep:*

13: /cgn2_6/ptcdata/1/pubpaa/US09_NEW_PUB.pep:*

14: /cgn2_6/ptcdata/1/pubpaa/US09_NEW_PUB.pep:*
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Listing first 45 summaries
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US-10-057-5487-8
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US-09-952-060-33
US-09-958-355-20
US-09-968-355-20
US-09-968-355-23
US-09-968-355-23
US-09-968-355-39
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Sequence 3, Appli
Sequence 18, Appli
Sequence 5, Appli
Sequence 20, Appli
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		0;								j., j., j.	ئر سز ئے،	¯≻≥	ָּסְלָּ קיל	Appl Appl Appl	֓֞֜֜֞֜֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓	dirit.	عَامَ مُ

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SOFTWARE: Patentin v
SEQ ID NO 8
LENGTH: 163
TYPE: PRT
ORGANISM: HIV-HXB2
US-09-735-487-8
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TITLE OF INVENTION: METHOD OF MANAGING THE OF TITLE OF INVENTION: HIV POSTITIVE BASED ON TITLE OF INVENTION: OF HUMAN HIV STRAINS
FILE REFERENCE: 1377-125p
CURRENT APPLICATION NUMBER: US/09/735,487
CURRENT FILING DATE: 2000-12-14
PRIOR APPLICATION NUMBER: 09/117,217
PRIOR APPLICATION NUMBER: 09/117,217
PRIOR FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 15
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                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/389,459
FILING DATE: 15-FEB-195
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/087,009
FILING DATE: 01-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/756,551A
FILING DATE: 08-JAN-2001
                                                                                                                                                                                                                                                           CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 08/987,867
                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/376,184
FILING DATE: 17-AUG-1999
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: ENCAPSIDATED RECOMBINANT VIRAL
TITLE OF INVENTION: NUCLEIC ACID AND METHODS OF MAKING AND
TITLE OF INVENTION: USING SAME
                                                                          ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: UAI-004CPDV2CN PELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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nes 9; Conserv
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                                   NAME: Lauro, Peter C. REGISTRATION NUMBER: 32,360
                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/9 FILING DATE: 09-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: UZIP: 02109
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                                                                                                                                                                                                                               CLASSIFICATION:
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100.0%; Pred. No.
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-756-551A-4
                                                      ; ORGANISM: Human immunodeficiency virus type US-10-003-035-18
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US-10-003-035-18
Sequence 18, Application US/10003035
Patent No. US20020155127A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LENGTH: 294
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus Type
US-09-827-822-3
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                                                                                          SOFTWARE: PatentIn version 3.1
SEQ ID NO 18
LENGTH: 492
TYPE: PRT
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
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                   Query Match
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                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/003,035
CURRENT FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: 09/585,599
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: PCT/US01/18238
PRIOR APPLICATION NUMBER: PCT/US01/18238
PRIOR FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 75
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TITLE OF INVENTION: GENETIC VACCINE AGAINST HUMAN IMMUNODEFICIENCY VIRUS
FILE REFERENCE: 22488-712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: PEPTIDES THAT BLOCK VIRAL INFECTIVITY TITLE OF INVENTION: AND METHODS OF USE THEREOF FILE REFERENCE: TRIPEP, 003A CURRENT APPLICATION NUMBER: US/09/827,822 CURRENT FILING DATE: 2001-04-06 PRIOR APPLICATION NUMBER: US/09/370,368 PRIOR EPLICATION UNMBER: US/09/370,368 PRIOR EPLICATION NUMBER: US/09/370,368 PRIOR EPLING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 275 amino acid
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0.57;
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                 Length 492;
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Best Local Similarity

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US-09-952-060-33; Sequence 33, Application US/09952060; Publication No. US20030044421A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Olmsted, Robert APPLICANT: Keith, Paula APPLICANT: Dryga, Sergey
                                                  FILE REFERENCE: 20747Y
CURRENT APPLICATION NUMBER: US/09/952,060
CURRENT FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: PCT/US01/28861
PRIOR FILING DATE: 2001-09-14
                                                                                                                                                                                                                                                             APPLICANT: Emini, Emilio A.
APPLICANT: Youll, Rima
APPLICANT: Bett, Andrew J.
APPLICANT: Chen, Ling
APPLICANT: Kaslow, David C
                                                                                                                                             APPLICANT: Casimiro, Danilo R.
TITLE OF INVENTION: ENHANCED FIRST GENERATION ADENOVIRUS
TITLE OF INVENTION: VACCINES EXPRESSING CODON OPTIMIZED HIV1-GAG, POL, NEF
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                   PRIOR APPLICATION NUMBER: 60/317,814 PRIOR FILING DATE: 2001-09-07
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TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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 APPLICATION NUMBER: 60/279,056
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Chen, Ling
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Shiver, John W.
Toner, Timothy J.
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US-09-968-355-20
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SEQ ID NO 20
LENGTH: 515
                                              CURRENT APPLICATION NUMBER: US/09/968,355
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: 60/236,273
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 26
                                                                                                                                               APPLICANT: Sakalian, Michael
APPLICANT: Hunter, Eric
TITLE OF INVENTION: Chimeric Retroviral Gag Genes and Screening Assays
FILE REFERENCE: UAB-100XC1
                                    SOFTWARE: PatentIn version 3.1
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359 KARVLAEAM 367

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: LENGTH: 500
: TYPE: PRT
: ORGANISM: Human immunodeficiency virus
: FEATURE:
: FEATURE:
NAME/KEY: MISC_FEATURE
: LOCATION: (1)..(500)
: OTHER INFORMATION: HIV (FS-) GAG amino acid sequence
US-09-968-355-26
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US-09-968-355-26
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US-09-952-060-33
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                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.1 SEQ ID NO 26
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Patent No. US20020094523A1
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Best Local
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CURRENT FILING DATE: 2001-09-28
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PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 38
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PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Sakalian, Michael
APPLICANT: Hunter, Eric
TITLE OF INVENTION: Chimeric Retroviral Gag
FILE REFERENCE: UAB-100XC1
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Similarity 100.0%;
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Pred. No.
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Pred. No.
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; FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)..(531)
OTHER INFORMATION: Ch3 amino acid sequence
US-09-968-355-23
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Best Local Similarity
"atches 9; Conservi
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                                                                                                    PRIOR APPLICATION NUMBER: 60/236,273
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 26
SOPTWARE: Patentin version 3.1
SEQ ID NO 17
                                                                                                                                                                                                                                                                                               Sequence 17, Application US/09968355 Patent No. US20020094523A1 GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.1
SEQ ID NO 23
LENGTH: 531
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                                                                                                                                                                                                                         APPLICANT: Hunter, Eric
TITLE OF INVENTION: Chimeric Retroviral Gag Genes and Screening Assays
FILE REFERENCE: UAB-100XC1
                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/968,355
CURRENT FILING DATE: 2001-09-28
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CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: 60/236,273
PRIOR FILING DATE: 2000-09-28
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APPLICANT: Hunter, Eric
TITLE OF INVENTION: Chimeric Retroviral Gag Genes and Screening Assays
FILE REFERENCE: UAB-100XC1
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                                                                     TYPE: PRT
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ORGANISM: Artificial Sequence
NAME/KEY: MISC_FEATURE LOCATION: (1)..(583)
                                       FEATURE:
                                                     ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                         LENGTH: 583
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Pred. No. 1.1;
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Pred. No.
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; Sequence 59, Application U; Patent No. US20020155127A1; GENERAL INFORMATION:
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            CURRENT APPLICATION NUMBER: US/09/952,060
CURRENT FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: PCT/US01/28861
PRIOR ELING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: 60/317,814
PRIOR FILING DATE: 2001-09-07
PRIOR FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: 60/279,056
PRIOR APPLICATION NUMBER: 60/279,056
PRIOR APPLICATION NUMBER: 60/279,056
PRIOR APPLICATION NUMBER: 60/233,180
PRIOR APPLICATION NUMBER: 60/233,180
PRIOR FILING DATE: 2000-09-15
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SEQ ID NO 59
LENCTH: 599
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local (
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APPLICANT: Coner, Timothy J.
APPLICANT: Casimiro, Imanilo R.
APPLICANT: Casimiro, Imanilo R.
TITLE OF INVENTION: ENHANCED FIRST GENERATION ADENOVIRUS
TITLE OF INVENTION: VACCINES EXPRESSING CODON OPTIMIZED
TITLE OF INVENTION: MODIFICATIONS
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Emini, Emilio A.
APPLICANT: Youil, Rima
APPLICANT: Bett, Andrew J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/003,035
CURRENT FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: 09/585,599
PRIOR FILING DATE: 2000-06-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wang, Danher TITLE OF INVENTION: GENETIC VACCINE AGAINST HUMAN IMMUNODEFICIENCY VIRUS FILE REFERENCE: 22488-712
                                                                                                                                                                                                              FILE REFERENCE: 20747Y
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SEQ ID NOS:
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Chen, Ling
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100.0%;
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Pred. No.
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APPLICANT: Eberle, Josef
APPLICANT: Brunn, Albrecht V.
APPLICANT: Hauser, Hans-Peter
TITLE OF INVENTION: RETROVIRUS FROM HIV GROUP AND ITS USE
FILE REFERENCE: 05495.0001-04
CURRENT APPLICATION NUMBER: US/09/886,156
CURRENT FILING DATE: 1908-07-02
PRIOR APPLICATION NUMBER: US/09/109,916
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: DE P 42 33 646.5
PRIOR APPLICATION NUMBER: DE P 42 35 718.7
PRIOR APPLICATION NUMBER: DE P 42 35 718.7
PRIOR APPLICATION NUMBER: DE P 42 44 541.8
PRIOR FILING DATE: 1992-10-02
PRIOR FILING DATE: 1992-10-22
PRIOR APPLICATION NUMBER: DE P 42 44 541.8
PRIOR FILING DATE: 1992-12-30
PRIOR APPLICATION NUMBER: DE P 43 18 186.4
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; OTHER INFORMATION: Codon optimized gag-IA pol fusion
US-09-952-060-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LENGTH: 498
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-886-156-59
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US-09-886-156-60
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Guertler, Lutz G.

APPLICANT: Eberle, Josef

APPLICANT: Brunn, Albrecht V.

APPLICANT: Knapp, Stefan

APPLICANT: Knapp, Stefan

APPLICANT: Hauser, Hans-Peter

TITLE OF INVENTION: RETROVIRUS FROM HIV GROUP AND ITS USE

FILE REFERENCE: 05495,0001-04

CURRENT APPLICATION NUMBER: US/09/886,156

CURRENT FILING DATE: 2001-06-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 59, Application US/09886156 Patent No. US20020155428A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 80.0
Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                                                                                                                                        Sequence 60, Application US/09886156 Patent No. US20020155428A1
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NUMBER OF SEQ ID NOS:
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77.8%;
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Pred. No. 7
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3.3;
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PRIOR APPLICATION NUMBER: DE P 42 33 646.5
PRIOR FILING DATE: 1992-10-06
PRIOR FILING DATE: 1992-10-02
PRIOR FILING DATE: 1992-10-22
PRIOR PILING DATE: 1992-10-22
PRIOR APPLICATION NUMBER: DE P 42 44 541.8
PRIOR APPLICATION NUMBER: DE P 43 18 186.4
PRIOR APPLICATION NUMBER: DE P 43 18 186.4
PRIOR FILING DATE: 1993-06-01
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PATENTIN NOS: 67
SOFTWARE: PATENTIN NOS: 67
CORGANISM: Human immunodeficiency virus
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Search completed: March 13, 2003, 18:54:48 Job time: 9.54545 secs
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                                                                             358 KAKILAEAM 366
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                                                                                                                   2 KARVLAEAM 10
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77.8%;
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Post-processing: Minimum Match 0%
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Maximum DB
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Perfect score:
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seq length: 2000000000
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Match Length
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      // Cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep: *
// Cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep: *
// Cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep: *
// Cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep: *
// Cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep: *
// Cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep: *
// Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep: *
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// Cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep: *
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US-10-003-035-18
US-09-991-258-5
US-09-952-060-335-26
US-09-968-355-26
US-09-968-355-27
US-09-968-355-27
US-09-968-355-27
US-09-968-355-27
US-09-968-355-27
US-09-968-355-27
US-09-952-060-35
US-09-861-289-41
US-09-861-289-41
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US-10-057-505-4
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US-09-827-822-3
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53.938 Million cell updates/sec
Sequence 130, App
Sequence 4, Appli
Sequence 8, Appli
Sequence 3, Appli
Sequence 18, Appli
Sequence 5, Appli
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AT TOWNSHIP	US-09-827-822-9	US-09-801-368-360	US-09-815-242-13762	US-09-815-242-10316	US-09-841-132-447	US-09-738-626-5378	US-09-764-898-187	US-09-947-387-29	US-10-112-894-2	US-09-808-602-81	US-09-808-602-84	US-09-808-602-80	US-09-808-602-8	US-09-808-602-13	US-09-808-602-83	US-09-815-242-13826	US-09-886-159-60	US-09-886-159-59	US-09-886-149-60	US-09-886-149-59	US-09-886-150-60	US-09-886-150-59	US-09-886-156-60	US-09-886-156-59	US-09-827-822-4	US-09-827-822-5
	Sequence 9, Appli	Sequence 360, App	Sequence 13762, A	10316	Sequence 447, App	Sequence 5378, Ap	187,	Seguence 29, Appl	Sequence 2, Appli	81,	Sequence 84, Appl	80,	8, 4	Sequence 13, Appl	Sequence 83, Appl	Sequence 13826, A	60,	59,	Sequence 60, Appl	59,	60,	Sequence 59, Appl	Sequence 60, Appl	•	Sequence 4, Appli	Sequence 5, Appli

ALIGNMENTS

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: AURORA BIOSCIENCES CORPORATION
APPLICANT: TSIEN, ROGER
APPLICANT: HELM, ROGER
                                                                                                                                                                          ; Sequence 4, Application US/10057505
; Patent No. US20020164674A1
                                                                                                                                                                                                                      RESULT 2
US-10-057-505-4
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 130
LENGTH: 219
                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 8; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Sheppard, Paul O.
APPLICANT: Presnell, Scott R.
TITLE OF INVENTION: MAMMALIAN SECRETED PROTEINS
FILE REFERENCE: 00-41
CURRENT APPLICATION NUMBER: US/09/893,737
CURRENT FILING DATE: 2001-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CUMRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 60/215,446
PRIOR FILING DATE: 2000-06-30
NUMBER OF THE PRIOR DATE: 2000-06-30
APPLICANT: CUBITT, Andrew TITLE OF INVENTION: TANDEM FLUORESCENT PROTEIN CONSTRUCTS FILE REFERENCE: REGEN1260-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                         1 EKARVLAEAA 10
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52 EKSRLLAEAA 61
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Pred. No. 1.5;
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NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin Ve.
SEQ ID NO 8
LENGTH: 163
TYPE: PRT
ORGANISM: HIV-HXB2
US-09-735-487-8
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US-09-756-551A-4
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; OTHER INFORMATION: Linker molety
US-10-057-505-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: METHOD OF MANAGING THE TITLE OF INVENTION: HIV POSTITIVE BASED ON TITLE OF INVENTION: OF HUMAN HIV STRAINS FILE REFERENCE: 1377-125P CURRENT APPLICATION NUMBER: US/09/735,487 CURRENT FILING DATE: 2000-12-14 PRIOR APPLICATION NUMBER: 09/117,217 PRIOR FILING DATE: 1998-07-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-735-487-8
                                                                                                                                                                   Sequence 4, Application US/09756551A Patent NO. US2002005176BA1
GENERAL INFORMATION:
APPLICANT: C. MOITOW et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/09735487 Patent No. US20020042679A1
GENERAL INFORMATION:
APPLICANT: de BETHUNE, Marie-Pierre APPLICANT: HERTOGS, Kurt APPLICANT: PAUWELS, Rudi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 09/396,003
PRIOR FILING DATE: 1999-09-13
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                           TITLE OF INVENTION: ENCAPSIDATED FITTLE OF INVENTION: NUCLEIC ACID & TITLE OF INVENTION: USING SAME NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD STREET: 28 STATE STREET
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CURRENT FILING DATE: 2002-01-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 10
TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 8; Conserv
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mes 8; Conserv
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MASSACHUSETTS
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                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     METHOD OF MANAGING THE CHEMOTHERAPY OF PATIENTS WHO ARE HIV POSTITIVE BASED ON THE PHENOTYPIC DRUG SENSITIVITY
                                                                                                         ENCAPSIDATED RECOMBINANT VIRAL NUCLEIC ACID AND METHODS OF MAKING AND USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.5%; Score 35; 100.0%; Pred. No.
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US-09-827-822-3
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                                                                                                                                        TITLE OF INVENTION: PEDTIDES THAT BLOCK VIRAL INFECTIVITY
TITLE OF INVENTION: AND METHODS OF USE THEREOF
FILE REFERENCE: TRIPEP.003A
CURRENT APPLICATION NUMBER: US/09/827,822
CURRENT FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: US/09/370,368
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/09827822
Patent No. US20020091086A1
GENERAL INFORMATION:
APPLICANT: Anders Vahlne
Query Match
Best Local Similarity
Matches 8; Conserv
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                                                                                       LENGTH: 294
TYPE: PRT
ORGANISM: Human
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: LAUTO, PETER 32,360
REGISTRATION NUMBER: 32,360
REFERENCE/DOCKET NUMBER: UAI-004CPDV2CN
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/389,459
FILING DATE: 15-FEB-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 275 amino acids
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APPLICATION NUMBER: 08/9
FILING DATE: 09-DEC-1997
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APPLICATION NUMBER: 08/376,184
FILING DATE: 17-AUG-1999
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           230 KARVLAEA 237
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(617) 742-4214
79.5%; Score 35; DB 10; ilarity 100.0%; Pred. No. 8.7; Conservative 0; Mismatches 0
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                                                                                       Immunodeficiency Virus Type 1
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08-JAN-2001
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100.0%; Pr
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Pred. No.
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Indels
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; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type
US-10-003-035-18
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APPLICANT: Olmsted, Robert
APPLICANT: Keith, Paula
APPLICANT: Dryga, Sergey
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
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                                                                                                                                                                                                                                                                        APPLICANT: Davis, Nancy
APPLICANT: Swanstrom, Ronald
APPLICANT: Swanstrom, Ronald
TITLE OF INVENTION: ALPHAVIRUS VECTORS AND VIROSOMES WITH MODIFIED HIV GENES FOR USE
TITLE OF INVENTION: VACCINES
FILE REFERENCE: 01113.000103
CURRENT APPLICATION NUMBER: US/09/991,258
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 09/902,537
PRIOR APPLICATION NUMBER: 09/902,537
PRIOR FILING DATE: 2000-07-09
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
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CURRENT FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: 09/585,599
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: PCT/US01/18238
PRIOR FILING DATE: 2001-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wang, Danher TITLE OF INVENTION: GENETIC VACCINE AGAINST HUMAN IMMUNODEFICIENCY VIRUS FILE REFERENCE: 22488-712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 75
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                                                                                                  LENGTH: 492
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence;
OTHER INFORMATION: synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               339 KARVLAEA 346
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Caley, Ian
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                 Conservative
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             score 35; DB 1
s; Pred. No. 16;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-952-060-33
                                                                                                           SOFTWARE: Pate
SEQ ID NO 26
LENGTH: 500
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 26, Application US/09968355
Patent No. US2002094523A1
GENERAL INFORMATION:
APPLICANT: Sakalian, Michael
APPLICANT: Hunter, Eric
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Best Local S
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Publication No.
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APPLICANT: Casimiro, Danilo R.
TITLE OF INVENTION: ENHANCED FIRST GENERATION ADENOVIRUS
TITLE OF INVENTION: VACCINES EXPRESSING CODON OPTIMIZED HIV1-GAG,
TITLE OF INVENTION: MODIFICATIONS
FILE REFERENCE: 20747Y
                                                                                                                                                                                                                                             APPLICANT: Hunter, Eric TITLE OF INVENTION: Chimeric Retroviral Gag Genes and Screening Assays FILE REFERENCE: UAB-100XC1 CURRENT APPLICATION NUMBER: US/09/968,355 CURRENT FILING DATE: 2001-09-28 PRIOR APPLICATION NUMBER: 60/236,273 PRIOR APPLICATION NUMBER: 60/236,273 PRIOR FILING DATE: 2000-09-28 PRIOR PRIOR FILING DATE: 2000-09-28 PRIOR 
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PRIOR FILTING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR APPLICATION NUMBER: PCT/US01/28861
PRIOR FILING DATE: 2001-09-14
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PRIOR FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: 60/279,056
PRIOR FILING DATE: 2001-03-27
PRIOR FILING DATE: 2001-03-27
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TYPE: PRT
ORGANISM: Artificial Sequence
                                  ORGANISM: Human immunodeficiency virus FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: MISC_FEATURE
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Shiver, John W.
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100.0%; pr
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Pred. No.
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, NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(515)
; OTHER INFORMATION: Ch3a amino acid sequence
US-09-968-355-20
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Best Local Similarity
""" B; Conserve
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; OTHER INFORMATION: HIV (FS-) GAG amino acid sequence
US-09-968-355-26
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                                                                                                                           SOFTWARE: PatentIn version 3.1
SEQ ID NO 23
LENGTH: 531
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                   Sequence 23, Application US/09968355 Patent No. US20020094523A1 GENERAL INFORMATION:
Query Match
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Best Local :
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APPLICANT: Hunter, Eric
TITLE OF INVENTION: Chimeric Retroviral Gag Genes and Screening Assays
FILE REFERENCE: UAB-100XC1
CURRENT APPLICATION NUMBER: US/09/968,355
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: 60/236,273
PRIOR APPLICATION NUMBER: 60/236,273
PRIOR FILING DATE: 2000-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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CURRENT APPLICATION NUMBER: US/09/968,355
CURRENT FILING DATE: 2001-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Sakalian, Michael
APPLICANT: Hunter, Eric
TITLE OF INVENTION: Chimeric Retroviral Gag
                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 26
                                               FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)..(531)
OTHER INFORMATION: Ch3
                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 515
TYPE: PRT
ORGANISM: Artificial Sequence
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                                             Ch3 amino acid sequence
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 Score 35;
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17;
 DB 10;
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 Length 531;
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359 KARVLAEA 366

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RESULT 12
US-09-968-355-17
; Sequence 17, Ap
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; LOCATION: (1)..(583)
OTHER INFORMATION: Chimera 4 amino acid sequence
US-09-968-355-17
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 17
LENGTH: 583
TYPE: PRT
                                                                                                                                                                    SOFTWARE: PatentIn version 3.1
SEQ ID NO 59
LENGTH: 599
                                                                                                                                                                                                                                                                                                                                                                               Sequence 59, Application US/10003035 Patent No. US20020155127A1 GENERAL INFORMATION:
                               Matches
                                            Query Match
Best Local
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Matches 8; Conserv
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Best Local Similarity
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CURRENT FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: 09/585,599
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: PCT/US01/18238
                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wang, Danher TITLE OF INVENTION: GENETIC VACCINE AGAINST HUMAN IMMUNODEFICIENCY VIRUS FILE REFERENCE: 22488-712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. US20020094523A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/968,355
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: 60/236,273
PRIOR FILING DATE: 2000-09-28
                                                                                                                                                                                                                       PRIOR FILING DATE: 2001-06-04 NUMBER OF SEQ ID NOS: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Sakalian, Michael
APPLICANT: Hunter, Einer
TITLE OF INVENTION: Chimeric Retroviral Gag Genes and Screening Assays
FILE REFERENCE: UAB-100XC1
                                                                                                           FEATURE:
OTHER INFORMATION: Gag-PI
                                                                                                                                        ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence FEATURE:
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                               Local Similarity
les 8; Conserv
2 KARVLAEA 9
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                                            79.5%;
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                                              Score 35;
Pred. No.
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Pred. No. 19;
0; Mismatches
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Mismatches
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19;
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                                                           Length 599;
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; APPLICANT: Zhao, L.
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin
; FILE REFERENCE: 600.438US1
; CURRENT APPLICATION NUMBER: US/09/860,846
; CURRENT FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: 09/105,537
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEO ID NOS: 43
; SOFTWARE: FastSEO for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 928
; TYPE: PRT
; ORGANISM: Streptomyces venezuelae
US-09-860-846-41
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US-09-952-060-35
; Sequence 35, Application US/09952060
; Publication No. US20030044421A1
; GENERAL INFORMATION:
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; Sequence 41, Application US/09860846
; Patent No. US20020164742A1
; GENERAL INFORMATION:
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Best Local S
Matches 8
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 35
LENGTH: 1350
Query Match
Best Local Similarity
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APPLICANT: Casimiro, Danilo R.

APPLICANT: Casimiro, Danilo R.

TITLE OF INVENTION: ENHANCED FIRST GENERATION ADENOVIRUS

TITLE OF INVENTION: VACCINES EXPRESSING CODON OPTIMIZED HIV1-GAG, POL, NEF AND

TITLE OF INVENTION: MODIFICATIONS

FILE REFERENCE: 20747Y

CURRENT APPLICATION NUMBER: US/09/952,060

CURRENT FILING DATE: 2001-09-14

PRIOR APPLICATION NUMBER: PCT/US01/28861

PRIOR APPLICATION NUMBER: 60/317,814

PRIOR APPLICATION NUMBER: 60/317,814

PRIOR APPLICATION NUMBER: 60/279,056

PRIOR APPLICATION NUMBER: 60/279,056

PRIOR APPLICATION NUMBER: 60/279,056

PRIOR FILING DATE: 2001-03-27

PRIOR FILING DATE: 2001-03-27

PRIOR FILING DATE: 2001-03-27

PRIOR FILING DATE: 2001-03-27
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APPLICANT: Youil, Rima
APPLICANT: Bett, Andrew J.
APPLICANT: Chen, Ling
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
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ORGANISM: Artificial Sequence
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Toner, Timothy J.
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  75.0%;
77.8%;
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  Score 33;
Pred. No.
  DB
84;
                       9;
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                     Length 928;
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Matches 7; Conservative 1; Mismatches 1; Indels

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Search completed: March 13, 2003, 18:54:47
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Sequence:
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O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA FLJ25373 fis, clone TST01951.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606;
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099PH8;
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Q8XUU1;
01-MAR-2002
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"Towards a Catalog of Human Genes and Proteins: Sequencing and Analysis of 500 Novel Complete Protein Coding Human cDNAs.";
Genome Res. 11:422-435(2001).

EMBL: AL136774; CAB66708 1; -.

Hypothetical protein.

SEQUENCE 1663 AA; 180826 MW; 62E1441FEF5C4DEE CRC64;
                                                                                                                                                                                              Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases EMBL; AF288572; AAG60016.1; -. SEQUENCE 131 AA; 14538 MW; 7FB9C3E7242EB424 CRC64;
                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
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Mammalia; Eutheria;
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequ
01-MAR-2002 (TrEMBLrel. 20, Last ann
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"Genome sequence of the plant pathogen Ralstonia solanacearum.";

Nature 415.497-502(2002).

EMBL; AL646073; CAD16803.1; -.

Hypothetical protein; Complete proteome.

SEQUENCE 264 AA; 28781 MW; F68F861312DD3F61 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUB-HEALTHY LIVER;
MEDLINB-20010026; PubMed-10540161;
Hodgson P.D., Grant M.D., Michalak T.I.;
Perforin and Fas/Fas ligand-mediated cy:
chronic woodchuck viral hepatitis.";
Clin. Exp. Immunol. 118:63-70(1999).
EMBL; AF152368; AAD38387.1;
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InterPro; IPR000478; TNF_family.
Pfam; PF00229; TNF; 1.
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Mammalia; Eutheria;
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MEDLINE-21681879; PubMed-11823852;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein RSc3094.
RSC3094 OR RS00547.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Marmota.
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                                                                  KELAELRES
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   KELPELRES
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19274 MW;
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Rodentia;
                                                                                                                                                                72.0%;
88.9%;
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ia; beta subdivision; Ralstonia
                                                                                                                                 0;
                                                                                                                                 Score 36; DB Pred. No. 33; 0; Mismatches
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ID OGLJE3

AC 09LJE3;
AC 09LJE3;
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DCT-2000 (TrEMBLrel. 19, Last annotation update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Genomic DNA, chromosome 3, P1 clone: MRP15.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Spermatophyta; Brassicales; Brassicaceae; Arabidopsis.
RESULT OF REAL PROPERTY OF REAL PROPERTY
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Best Local S
Matches 6
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"A set
the 8 M
Mol. Mi
[4]
                     Redenbach M., Kieser H.M., Denapaite D., Eichner A
Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic a
the 8 Mb Streptomyces coelicolor A3(2) chromosome.
Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                      Murphy L., Harris D.;
Submitted (SEP-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
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                                                                                                                                                      STRAIN-A3(2)
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Actinomycetales;
NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces coelicolor.
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                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                              Submitted
                                                                                                                                                                                                                                                 Thomson N.R.,
                                                                                                                                                                                                                                                                    STRAIN-A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20363099;
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                                                                                                                                   MEDLINE-97000351; PubMed-8843436;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              uence features of the region and BAC clones.";
Res. 7:217-221(2000).
L; AP000603; BAB01755.1; -.
UENCE 265 AA; 30326 MW;
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                                                                                                                                                                                                                            .R., Parkhill
(SEP-1999) to
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e EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                        EMBL/GenBank/DDBJ
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EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last annotation update)
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Pred. No. 53;
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                                              genetic and hromosome.";
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01-MAY-1999 (TrEMBLrel. 11

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Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                 chytrid Piromyces sp. E2.";

Mol. Microbiol. 30:1017-1027(1998).

-I- CATALYTIC ACTIVITY: 2.3-DIHYDROXYISOVALERATE + NADP(+) = 2-
ACETOLACTATE + NADPH (ALSO: 2.3-DIHYDROXYACID-3-METHYLVALERATE
ACETOLACTATE + NADPH (ALSO: 4.3-DIHYDROXYACID-3-METHYLVALERATE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:141-147(2002).
                                                                                                                                                                                                      HSSP; 001292; 10MG.
InterPro; IPR000506; AcH_isomrdctse.
Pfam; PF01450; 11VC; 1.
TIGRFAMS; TIGR00465; ilvC; 1.
                                                                                                                                                                                                                                                                          NADP(+) = 2-ACETO-2-HYDROXYBUTYRATE + NADPH).
EMBL; Y16743; CAA76356.1; -.
HSSP; Q01292; LQMG.
                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Akhmanova A., Vo
Hackstein J.H.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=73868;
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Neocallimasticaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Piromyces sp.
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SEQUENCE 28
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SMART; SM00331; PP2C_SIG;
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                                                                                                                                                                                 Isomerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cytosolic enzymes with a mitochondrial chytrid Piromyces sp. E2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE + 99141007; PubMed = 9988478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQUENCE FROM N.A.
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                                                                           Local
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  1 KELAELRES 9
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                                                    Similarity
8; Conserv
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8; Conserv
                                                                                                                                                    NADP; Oxidoreductase.
352 AA; 39453 MW; 8
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                                                      Conservative
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88.9%;
                                                                         72.0%;
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21,
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Last annotation update)
(EC 1.1.1.86).
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                                                                           Score 36;
Pred. No.
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Pred. No.
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                                                      Mismatches
                                                                                                                                                       8E2056BC934C1C14 CRC64;
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57;
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                                                                                                        Length 352
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RESULT DESCRIPTION OF THE PROPERTY OF THE PROP
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                                                                                                                              Query Match
Best Local S
Matches 8
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Best Local
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01-OCT-2000 (TrEMBLrel. 1
01-JUN-2002 (TrEMBLrel. 2
Hypothetical protein SCO
SCO2524 OR SCC121.27C.
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STRAIN-A3(2) / Mid5;

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,

Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,

Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

Marren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Wing R.A., Yu Y., Soderlund C., Chen M., Kim
Saski C., Henry D., Oates R., Simmons J.;
"Rice Genomic Sequence.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Em
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzaae; Oryza.
NCBI_TaxID-39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8S5V4 PRELIMINARY; PRT; 876 AA. Q8S5V4; Q8S5V
                                                                                                                                                                                                                                                             Hypothetical protein. SEQUENCE 876 AA; 9
                                                                                                                                                                                                                                                                                                                                Submitted (APR-2002) to the EMBL; AC104427; AAM19115.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete genome sequence of the model actinomycete coellcolor A3(2)."; coellcolor A3(2)."; 141-147(2002).

EMBL: AL137166; CAB69745.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptomyces coelicolor.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9L2F9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical
253
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                                                               KELAELRESTS
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KELKELKEITS
                                                                                                                              8; Conserv
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                                                                                                                                  Conservative
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                                                               11
                                                                                                                                                                                                                                                                    97835 MW;
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                                                                                                                                                              72.08;
72.78;
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63.6%;
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el. 15, Last sequence update)
el. 21, Last annotation update)
SCO2524.
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                                                                                                                                                                                                                                                                 26AE76D87C3E0180 CRC64;
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                                                                                                                                  Mismatches
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                                                                                                                                                          36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Embryophyta; Tracheophyta; a; Poales; Poaceae;
                                                                                                                    .9e+02;
2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H.-R.,
                                                                                                                                                                                                                                                                                                                                                                       databases
                                                                                                                                                                                          Length 876;
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                                                                                                                              Indels
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RESULT OF THE CASE OF THE CASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RX MEDLINE-2019606; PubMed=10731132;
RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfelffer B.D.,
RA Handon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfelffer B.D.,
RA Handon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfelffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Becson K.Y., Benos P.V., Berman B.P., Bhandarl D., Bolshakov S.,
RA Becson K.Y., Benos P.V., Berman B.P., Bhandarl D., Bolshakov S.,
RA Becson K.Y., Busm D.A., Butler H., Godieu E., Center A., Chandra I.,
RA Cherry J.M., Cauley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cauley S., Dahlke C., Berriater S., Fleischmann W.,
RA Gepablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dletz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Herris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Kimmel B.E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Alazson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Stapleton M., Strong R., Sun E.,
RA Shue B.C., Stapleton M., Strong R., Sun E.,
RA Shue B.C., Stapleton M., Strong R., Sun E.,
RA Shue B.C., Stapleton M., Strong R., Sun E.,
RA Shue B.C., Stapleton M., Venter T., Wang A.H., Wang X.,
Ra Shue B.C., Stapleton M., Venter J.C.,
Ra Shue S., Sa
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O9V309
O1-MAY-2000 (TrEMBLrel. 13, C
O1-MAY-2000 (TrEMBLrel. 13, L
O1-UN-2002 (TrEMBLrel. 21, L
CG15274 protein
GABA-B-R1 OR BG:DS00929.6 OR
STRAIN-BERKELEY;
Celniker S.E., Agbaya
Butenhoff C., Champe
                                                                                                                                                              MEDLINE-99403001; PubMed-10471707;
Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T.,
Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,
Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K.,
Celniker S., Rubin G.M.;
"An exploration of the sequence of a 2.9-Mb region of the genome of
Drosophila melanogaster: the Adh region.";
Genetics 153:179-219(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GABA-B-RÌ OR BG:DS00929.6 OR CG15274.
Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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   Agbayani /
Champe M.,
   A., Arcaina
, Chavez C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation updat
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   Baxter E., Blazej
M., Ciesiolka L., I
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RA Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
RA Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
RA Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
RA Sethi H., Snir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,
RI Sibmitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AE003646; AAF53431.1; -.
RE EMBL; AE003641; AAF44910.1; -.
RE EMBL; AE003411; AAF44910.1; -.
RE EMBL; AE003412; GABA-B-R1.
RI InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR00037; GABA-B.
ROB Pfam; PF00287; Na_K-ATPase_beta.
ROB Pfam; PF00287; Na_K-ATPase_beta.
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Yamada K., Banh J., Banno F., Dale J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Yamamura Y., Yu G., Onodera C.S., Quach H.L., Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
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Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation updat
Hypothetical 13.5 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Full Length cDNA of gene At1g06525.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ
EMBL; AY056146; AAL07225.1;
InterPro; IPR001230; Prenyl_site.
PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-MAR-2001
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STRAIN-ACC 15692 / PAO1;

MEDLINE-20437337; PubMed-10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowallk D.J., Lagrou M.

Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

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opportunistic pathogen.";

Nature 406:959-964(2000).

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MEROPS. SA1 004.
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Bailey J., Cook L.J., Kilmer-Barber R., Swanston E.,
Solnica-Krezel L., Lohman K.N., Dove W.F., Dee J., Anderso
"Identification of three genes expressed primarily during
in Physarum polycephalum.",
Arch. Microbiol. 172:364-376(1999).
EMBL; AJ133501; CAB39170.1; -.
RON_TER. 1
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Putative type II myosin heavy chain (Fragment).
MYND.
                                                                                                     Protease;
SEQUENCE
                                                                                                                                                                                              InterPro; IPR001478; PD2.
InterPro; IPR004447; Protease_Cterm.
InterPro; IPR003581; TSPC.
Pfam; PF00595; PD2; 1.
SMART; SM00228; PD2; 1.
SMART; SM00245; TSPC; 1.
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01-MAR-2001 (TrEMBLrel. 16,
01-JUN-2002 (TrEMBLrel. 21,
probable carboxyl-terminal p
                                                                                                                                                    TIGRFAMS; TIGR00225; prc; 1. PROSITE; PS50106; PDZ; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         436
                       1.4e+02;
                                                 DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 317
                                              Length 436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anderson
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Conservative

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Mismatches

Indels

0;

Gaps

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91

KELAELRESTS EDFAELQESTS 101

11

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RESULT 15
Q9VNM2
ID Q9VNM
AC Q9VNM
DT 01-M2
DT 01-M2
DT 01-M2
DT 01-M3
DT 0
В
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RA Addms D.D., Celniker S.E., Hichtrad S., Ashburner M., Henderson S.N.,
RA Goorge R.A., Lewis S.E. Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Preiffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Gebriy J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gebios B., Delcher A., Deng Z., Mays A.D., Dew T., Dietz S.M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Galbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gann P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gann P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Wel M.-H., Ibeysam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Merkubov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkubov G., Wilshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkubov G., Wilshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkubov G., Wilshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkubov G., Wilshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Rainert K., Remington K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Rainert K., Remington K.A., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Stapleton M., Skupski M.P., Smith T.,
RA Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Stapleton M., Skupski M.P., Smith T.,
RA Rainer E., Saveri J. Shon M., Skupski M.P., Smith T.,
Rang J.-Y., Wassasman D.A., Welshinscok G.M., Welssenbach J.,
Rang J.-Y., Wassasman D.A., Welshin M., Shang G., Zhao Q., Zheng J.,
Rang J.-Y., Wassasman J., We
                                                                                                                                      Ouery Match
Best Local S
Matches 8
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
CG15589 protein.
CG15589.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                          "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
EMBL; AE0003600; AAF51908.1; -.
FlyBase; FBgn0037409; CG15589.
SEQUENCE 482 AA; 53353 MW; E3C7E9ECC4A1226A CR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-20196006;
413
                                                              1 KELAELRESTS 11
KELNELRKPTS 423
                                                                                                                                          Similarity
8; Conserv
                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=10731132;
                                                                                                                                                                           70.08;
72.78;
                                                                                                                                                                       Score 35; DB 5;
Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                             E3C7E9ECC4A1226A CRC64;
                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  482
                                                                                                                                                                                                        DB 5; Length 482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  À
                                                                                                                                   0;
                                                                                                                                   Gaps
                                                                                                                                   0;
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Search completed: March 13, 2003, 18:51:53 Job time: 25.8 secs